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OM protein - protein search, using sw model

Run on: February 26, 2004, 11:58:57, Search time 23 Seconds

(without alignments)
767.656 Million cell updates/sec

Title: US-09-401-636-8

Perfect score: 1856

Sequence: 1 EPHHHHTLSPESGPVTI.....HEALPGKTLKSLHYAAGN 342

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Database: Issued Patents PA:*

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	989	53.3	426	1	US-08-336-583-2
2	989	53.3	426	5	PCT-US95-13795-2
3	972	52.4	431	4	US-09-479-614-14
4	972	52.4	496	4	US-09-479-614-29
5	972	52.4	496	4	US-09-479-614-29
6	673	36.3	561	3	US-09-192-545-2
7	579	31.2	113	2	US-08-232-539D-56
8	548.5	29.6	109	4	US-08-466-163B-1
9	548.5	29.6	109	4	US-08-802-096-1
10	538	29.0	106	2	US-08-232-539D-54
11	512	27.6	334	2	US-08-646-981-16
12	508	27.4	119	2	US-08-464-025A-1
13	501.5	27.0	331	2	US-08-646-981-17
14	492.5	26.5	450	2	US-08-788-800-12
15	492.5	26.5	469	2	US-07-934-373C-23
16	492.5	26.5	469	2	US-08-437-642B-23
17	492.5	26.5	469	4	US-08-146-206C-23
18	492.5	26.5	469	4	US-09-705-686-23
19	490.5	26.4	118	3	US-08-466-151-1
20	490	26.4	333	1	US-08-436-463-6
21	490	26.4	333	1	US-08-024-253-6
22	488	26.3	530	3	US-08-477-460B-4
23	488	26.3	530	3	US-08-379-516-4
24	488	26.3	530	3	US-09-329-916-4
25	488	26.3	530	3	US-08-485-372A-4
26	488	26.3	530	4	US-09-409-006A-4
27	488	26.3	530	4	US-08-484-681-4

28	488	26.3	530	5	PCT-US93-07422-4	Sequence 4, Appl
29	486.5	26.2	451	4	US-09-472-087-70	Sequence 70, Appl
30	486.5	26.2	463	4	US-09-472-087-1	Sequence 1, Appl
31	486.5	26.2	463	4	US-09-472-087-4	Sequence 4, Appl
32	486.5	26.2	463	4	US-09-472-087-63	Sequence 63, Appl
33	486.5	26.2	463	4	US-09-472-087-68	Sequence 68, Appl
34	486.5	26.2	464	4	US-09-472-087-2	Sequence 2, Appl
35	486.5	26.2	464	4	US-09-472-087-66	Sequence 66, Appl
36	480.5	25.9	463	4	US-09-472-087-64	Sequence 64, Appl
37	476.5	25.7	329	2	US-09-313-942-12	Sequence 12, Appl
38	476	25.6	337	2	US-08-761-272A-47	Sequence 47, Appl
39	476	25.6	443	5	PCT-US96-13152-4	Sequence 4, Appl
40	476	25.6	467	1	US-08-704-744-81	Sequence 81, Appl
41	476	25.6	467	3	US-08-523-894-8	Sequence 8, Appl
42	476	25.6	467	3	US-08-523-894-10	Sequence 10, Appl
43	476	25.6	467	3	US-08-523-894-12	Sequence 12, Appl
44	475.5	25.6	326	2	US-08-656-586-9	Sequence 9, Appl
45	468.5	25.2	552	5	PCT-US93-07832-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-08-336-583-2
Sequence 2, Appl
Patent No. 5628415
GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,583
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-583-2
Query Match 53.3%, Score 989, DB 1, Length 426;
Best Local Similarity 56.7%, Pred. No. 16-87, 84, Indels 4, Gaps 3;
Matches 185; Conservative 53; Mismatches 84; Indels 4; Gaps 3;
OY 18 VTIIPTVTLFSSCGPRGDAHSTTGLCTVSGFSPAKVHTWLVDSGAENLFPYTRP 77
DB 102 LNFIPVTLGFSSCGPVDVDTHTTGLCLISGIVPGDMETVWLVDGQATNIFPYTAG 161
OY 78 KREGQTFSLQSEVNTTQGMMSNTYTGKVGKNSIFEEDSRKCADSNPRGVSAYLRP 137

DB 162 TREGVNT-STHSELNITOGEMWSOKTYTCQVYOGFTFKDEARKSESDEPBGVTSYLSPP 220
QY 138 SPFDLFIKSPITITCLVVDLAPSKGTVNLTWRSRASKPVNSTRKEEKORNGTLVTSSTL 197
DB 221 SPDLVYHAKPKITCLVVDLATMEG-MNLTWRSEKPEVNPGLNKOHFNIGTITVSTL 279
QY 198 PVGTRDMIGETGYOCVTHPHLPRALMRSTYLPGRKLAPLEVYMLPPSPETGTR--TV 255
DB 280 PVNTDMWIGETGYOCVTHPHLPRKIVRSIAAPGRAPDYYLFLPREEGOTKDRVYL 339
QY 256 TCLIRGEYSEISVQMLFNNEEDHTGHHTTTRPOKHGTDSPFLYSRLVYKSIWEKGN 315
DB 340 TCLIQNFPPADISVQMLRNDSPIDQYTTTGPVHVSGRAPAFIFSRLEVSRAVMEQKN 399
QY 316 LVTGRVYHEALPGSRITLKSILHYSAG 341
DB 400 KFTQCVVHEALPGSRITLQKWSKTPG 425

RESULT 2
PCT-US95-13795-2
; Sequence 2, Application PC/TUS9513795
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13795
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-13795-2

Query Match 53.3%; Score 989; DB 5; Length 426;
Best Local Similarity 56.7%; Pred. No. 1e-87;
Matches 185; Conservative 53; Mismatches 84; Indels 4; Gaps 3;

DB 18 VTIIPTVTLFHSNCPDPRGDASTITQLCLVGFSPAKVHTVWLVDGQEAENLFPYTRP 77
QY 102 LNPFIPTVTLFHSNCPVGDTHITITQLCLISGYVPGMEVYTWLVDGQKATNIPFYTAG 161
DB 78 KREGGQTFSLQSEVNTTQGMSSNTYTCHVKNHSIFEDSRKCADSNPRGVSAVLSRP 137
QY 162 TREGVNT-STHSELNITOGEMWSOKTYTCQVYOGFTFKDEARKSESDEPBGVTSYLSPP 220
DB 138 SPFDLFIKSPITITCLVVDLAPSKGTVNLTWRSRASKPVNSTRKEEKORNGTLVTSSTL 197

DB 221 SPDLVYHAKPKITCLVVDLATMEG-MNLTWRSEKPEVNPGLNKOHFNIGTITVSTL 279
QY 198 PVGTRDMIGETGYOCVTHPHLPRALMRSTYLPGRKLAPLEVYMLPPSPETGTR--TV 255
DB 280 PVNTDMWIGETGYOCVTHPHLPRKIVRSIAAPGRAPDYYLFLPREEGOTKDRVYL 339
QY 256 TCLIRGEYSEISVQMLFNNEEDHTGHHTTTRPOKHGTDSPFLYSRLVYKSIWEKGN 315
DB 340 TCLIQNFPPADISVQMLRNDSPIDQYTTTGPVHVSGRAPAFIFSRLEVSRAVMEQKN 399
QY 316 LVTGRVYHEALPGSRITLKSILHYSAG 341
DB 400 KFTQCVVHEALPGSRITLQKWSKTPG 425

RESULT 3
US-09-479-614-14
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

Query Match 52.4%; Score 972; DB 4; Length 431;
Best Local Similarity 56.7%; Pred. No. 4.7e-86;
Matches 185; Conservative 52; Mismatches 85; Indels 4; Gaps 4;

DB 18 VTIIPTVTLFHSNCPDPRGDASTITQLCLVGFSPAKVHTVWLVDGQEAENLFPYTRP 77
QY 107 LNPFIPTVTLFHSNCPVGDTHITITQLCLISGYVPGMEVYTWLVDGQKATNIPFYTAG 166
DB 78 KREGGQTFSLQSEVNTTQGMSSNTYTCHVKNHSIFEDSRKCADSNPRGVSAVLSRP 137
QY 167 KREGVNT-STHSELNITOGEMWSOKTYTCQVYOGFTFKDEARKSESDEPBGVTSYLSPP 225
DB 138 SPFDLFIKSPITITCLVVDLAPSKGTVNLTWRSRASKPVNSTRKEEKORNGTLVTSSTL 197
QY 226 SPDLVYHAKPKITCLVVDLATMEG-MNLTWRSEKPEVNPGLNKOHFNIGTITVSTL 284
DB 198 PVGTRDMIGETGYOCVTHPHLPRALMRSTYLPGRKLAPLEVYMLPPSPETGTR--TV 255
QY 285 PVNTDMWIGETGYOCVTHPHLPRKIVRSIAAPGRAPDYYLFLPREEGOTKDRVYL 344
DB 256 TCLIRGEYSEISVQMLFNNEEDHTGHHTTTRPOKHGTDSPFLYSRLVYKSIWEKGN 315
QY 345 TCLIQNFPPADISVQMLRNDSPIDQYTTTGPVHVSGRAPAFIFSRLEVSRAVMEQKN 404
DB 316 LVTGRVYHEALPGSRITLKSILHYSAG 341
QY 405 VFTQCVVHEALPGSRITLQKWSKTPG 425

RESULT 4
US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric

TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
 FILE REFERENCE: P-1047
 CURRENT APPLICATION NUMBER: US/09/479,614
 CURRENT FILING DATE: 2000-01-07
 EARLIER APPLICATION NUMBER: 60/115,033
 EARLIER FILING DATE: 1999-01-07
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2
 LENGTH: 496
 TYPE: PRT
 ORGANISM: Felis catus
 US-09-479-614-2

Query Match 52.4%; Score 972; DB 4; Length 496;
 Best Local Similarity 56.7%; Pred. No. 5,8e-86;
 Matches 185; Conservative 52; Mismatches 85; Indels 4; Gaps 4;

QY 18 VTIIPTVYKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTWLVDOGAENLPYTRP 77
 DB 172 NMFIPTVYKLFHSSCNPLGDTSTIQLCLISGYVPGDMETWLVDOGKATNIPYTPAG 231
 QY 78 KREGGQTSLOSEVNTTGOQWMSNTYTCVHKHNSIFEDSSRKCADSNPGVATLSRP 137
 DB 232 KQEGKVT-STHSELNITQSEWVSQKTYTCQVYQGFTEHDARKCTESDPGVSTYLSPP 290
 QY 138 SPFDLFIKSPITTCVLVDLAPSKGTVALTWASRASKPVNSTRKEEKORNGTLVTSTL 197
 DB 291 SPDLVYHKSFKITCLVVDLANTDGM-LTWSRENGESVHPDMVKKTQYNGITVTSTL 349
 QY 198 PGTGDMWEGEYQCVTHPHLPRALMSTYTLPGKRLAPVYM-LPSPPE-ETGTTTIV 255
 DB 350 PVDATDWEGEYQCKVTHPDLPKDIVRSIAAPGRPPPEVYVFLPPEGEPTKDKVYL 409
 QY 256 TGLIRGYPSZISVQWLFNNBEDHTGHTTTRPOKHGTDSPSFYLSRMLVNSIWEKGN 315
 DB 410 TGLIQNFFPPDISVQWLFNDSFVTEQATTPHKAATGSPAFVFSRLVEBRADWEQRD 469
 QY 316 LVTGRVYHVALPGSRTLEKSLHYSAG 341
 DB 470 VFTQVYHVALPGFRTLKKSVSKNPG 495

RESULT 5

US-09-479-614-29
 Sequence 29, Application US/09479614
 Patent No. 6573372
 GENERAL INFORMATION:
 APPLICANT: McCall, Catherine
 APPLICANT: Weber, Eric
 TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
 FILE REFERENCE: P-1047
 CURRENT APPLICATION NUMBER: US/09/479,614
 CURRENT FILING DATE: 2000-01-07
 EARLIER APPLICATION NUMBER: 60/115,033
 EARLIER FILING DATE: 1999-01-07
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 29
 LENGTH: 496
 TYPE: PRT
 ORGANISM: Felis catus
 US-09-479-614-29

Query Match 52.4%; Score 972; DB 4; Length 496;
 Best Local Similarity 56.7%; Pred. No. 5,8e-86;
 Matches 185; Conservative 52; Mismatches 85; Indels 4; Gaps 4;

QY 18 VTIIPTVYKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTWLVDOGAENLPYTRP 77
 DB 172 NMFIPTVYKLFHSSCNPLGDTSTIQLCLISGYVPGDMETWLVDOGKATNIPYTPAG 231
 QY 78 KREGGQTSLOSEVNTTGOQWMSNTYTCVHKHNSIFEDSSRKCADSNPGVATLSRP 137

DB 232 KQEGKVT-STHSELNITQSEWVSQKTYTCQVYQGFTEHDARKCTESDPGVSTYLSPP 290
 QY 138 SPFDLFIKSPITTCVLVDLAPSKGTVALTWASRASKPVNSTRKEEKORNGTLVTSTL 197
 DB 291 SPDLVYHKSFKITCLVVDLANTDGM-LTWSRENGESVHPDMVKKTQYNGITVTSTL 349
 QY 198 PGTGDMWEGEYQCVTHPHLPRALMSTYTLPGKRLAPVYM-LPSPPE-ETGTTTIV 255
 DB 350 PVDATDWEGEYQCKVTHPDLPKDIVRSIAAPGRPPPEVYVFLPPEGEPTKDKVYL 409
 QY 256 TGLIRGYPSZISVQWLFNNBEDHTGHTTTRPOKHGTDSPSFYLSRMLVNSIWEKGN 315
 DB 410 TGLIQNFFPPDISVQWLFNDSFVTEQATTPHKAATGSPAFVFSRLVEBRADWEQRD 469
 QY 316 LVTGRVYHVALPGSRTLEKSLHYSAG 341
 DB 470 VFTQVYHVALPGFRTLKKSVSKNPG 495

RESULT 6

US-09-192-545-2
 Sequence 2, Application US/09192545
 Patent No. 6118044
 GENERAL INFORMATION:
 APPLICANT: Karyasuyama, Hajime
 APPLICANT: Konekawa, Hiromichi
 APPLICANT: Taya, Choji
 APPLICANT: Matsuo, Kunie
 TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their Use
 FILE REFERENCE: 795P79570
 CURRENT APPLICATION NUMBER: US/09/192,545
 CURRENT FILING DATE: 1998-11-13
 EARLIER APPLICATION NUMBER: JP HEI 9-313989
 EARLIER FILING DATE: 1997-11-14
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2
 LENGTH: 561
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: Description of Artificial Sequence: Designed heavy
 US-09-192-545-2

Query Match 36.3%; Score 673; DB 3; Length 561;
 Best Local Similarity 41.6%; Pred. No. 8,1e-57;
 Matches 147; Conservative 53; Mismatches 133; Indels 20; Gaps 7;

QY 2 FHHHHHTLSLPESGVTIIPPTVYKLFHSSCDPRGDAHSTIQLCLVSGF 51
 DB 211 FTCHVTHPSFMSRSTIIVRPVT---HSLSPMSYSIHRCPDPA-FSTIOLYCFYGH 265
 QY 52 SPKAVHTWLVDOGAENLPYTRPKREGQTSLOSEVNTTGOQWMSNTYTCVHKH 111
 DB 266 ILNDVSVSMAMDRETDLTLAGTVLKEE-GCLASTCSKANTTEQWMSSESTFCRTV 324
 QY 112 GSIFFDSSRKCADSNPGVATLSRPSPFDLFIKSPITTCVLVDLAPSKGVNLTWSRA 171
 DB 325 GVDYLAHTRKCPDHEKRAITLIPSPDLQNGAPKYLCLVLDSEK-VNAVYWNQE 383
 QY 172 SGKPVNSTRKEEKORNGTLVTSTLPVGTGDMWEGEYQCVTHPHLPRALMSTYKLP 231
 DB 384 KKTYSVASQWYTKRHNNAITSTISILPVAKWIMIGYGQCVDRPDPKPIVRSIT-LP 442
 QY 232 --GKTLAPRYVNLPSRPEHTGTTTTCVCLIRGYPSZISVQWLFNNBEDHTGHTTTRPQ 289
 DB 443 QVSQSAPEVYVFPPEESEDKRTLCLIQNFFPPDISVQWLFNGKLISSQHSSTTLP 502
 QY 290 KDHGTDSPSFYLSRMLVNSIWEKGNLTCRVYHVALPGSRTLEKSLHYSAGN 342
 DB 503 KNSGNSQGFIFSRLEVAKTWLTQKQFTQVYHVALPKPRLEKTIISTISG 555

RESULT 7

US-08-232-539D-56
Sequence 56, Application US/08232539D
Patent No. 5965709
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: IGE Antagonists
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-Apr-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Syvoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9861
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-232-539D-56

Query Match 31.2%; Score 579; DB 2; Length 113;
Best Local Similarity 98.2%; Pred. No. 1e-46;
Matches 109; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 122 CADSNPRGVSAVLSRSPFDLFIKSPITICLVVDLAPSKGTVNLWTSRASKGVNSTR 181
DB 1 CADSNPRGVSAVLSRSPFDLFIKSPITICLVVDLAPSKGTVNLWTSRASKGVNSTR 60

QY 182 KEKORNGTLVTSTLPVGTDMWIEGTYQCRVTHPHLPALMNSTTKLPg 232
DB 61 KEKORNGTLVTSTLPVGTDMWIEGTYQCRVTHPHLPALMNSTTKTSg 111

RESULT 8
US-08-466-163B-1
Sequence 1, Application US/08466163B
Patent No. 6329509
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26

PRIOR APPLICATION NUMBER: US 07/879,495

PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14

NUMBER OF SEQ ID NOS: 64

SEQ ID NO 1

LENGTH: 109

TYPE: PRT

ORGANISM: Homo sapiens

US-08-466-163B-1

Query Match 29.6%; Score 548.5; DB 4; Length 109;

Best Local Similarity 97.2%; Pred. No. 8.9e-46;

Matches 106; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 124 DSNPRGVSAVLSRSPFDLFIKSPITICLVVDLAPSKGTVNLWTSRASKGVNSTR 183

DB 1 DSNPRGVSAVLSRSPFDLFIKSPITICLVVDLAPSKGTVNLWTSRASKGVNSTR 60

QY 184 EKORNGTLVTSTLPVGTDMWIEGTYQCRVTHPHLPALMNSTTKLPg 232

DB 61 EKORNGTLVTSTLPVGTDMWIEGTYQCRVTHPHLPALMNSTTKTSg 108

RESULT 9

US-09-802-096-1
Sequence 1, Application US/09802096
Patent No. 6665939

GENERAL INFORMATION:

APPLICANT: Presta, Leonard G.

APPLICANT: Jardieu, Paula M.

TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)

FILE REFERENCE: P0718P2C3US

CURRENT APPLICATION NUMBER: US/09/802,096

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: US 08/405,617

PRIOR FILING DATE: 1995-03-15

PRIOR APPLICATION NUMBER: US 08/185,899

PRIOR FILING DATE: 1994-01-26

PRIOR APPLICATION NUMBER: PCT/US92/06860

PRIOR FILING DATE: 1992-08-14

PRIOR APPLICATION NUMBER: US 07/879,495

PRIOR FILING DATE: 1992-05-07

PRIOR APPLICATION NUMBER: US 07/744,768

PRIOR FILING DATE: 1991-08-14

NUMBER OF SEQ ID NOS: 64

SEQ ID NO 1

LENGTH: 109

TYPE: PRT

ORGANISM: Homo sapiens

US-09-802-096-1

Query Match 29.6%; Score 548.5; DB 4; Length 109;

Best Local Similarity 97.2%; Pred. No. 8.9e-46;

Matches 106; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 124 DSNPRGVSAVLSRSPFDLFIKSPITICLVVDLAPSKGTVNLWTSRASKGVNSTR 183

DB 1 DSNPRGVSAVLSRSPFDLFIKSPITICLVVDLAPSKGTVNLWTSRASKGVNSTR 60

QY 184 EKORNGTLVTSTLPVGTDMWIEGTYQCRVTHPHLPALMNSTTKLPg 232

DB 61 EKORNGTLVTSTLPVGTDMWIEGTYQCRVTHPHLPALMNSTTKTSg 108

RESULT 10

US-08-232-539D-54
Sequence 54, Application US/08232539D
Patent No. 5965709

GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.

TITLE OF INVENTION: IGE Antagonists

NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-Apr-1994
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 06/178583
FILING DATE: 07-Jan-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-232-539D-54

Query Match 29.0%; Score 538; DB 2; Length 106;
Best Local Similarity 98.1%; Pred. No. 8.9e-45;
Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 129 GVSAYISRSPPDLFRKSPPTTCLVVDLAPSKGTNLTWSASGKPVNHSRKEKQPN 188
DB 1 GVSAYISRSPPDLFRKSPPTTCLVVDLAPSKGTNLTWSASGKPVNHSRKEKQPN 60

QY 189 GILTVSTLPVGTWDWIEGETYQCRVTHPHLPALMRSTTKLPG 232
DB 61 GILTVSTLPVGTWDWIEGETYQCRVTHPHLPALMRSTTKISG 104

RESULT 11
US-08-646-981-16
Sequence 16, Application US/08646981
Patent No. 5852183
GENERAL INFORMATION:
APPLICANT: MAEDA, HIROAKI
APPLICANT: EDA, YASUYUKI
APPLICANT: KIMACHI, KAZUHIKO
APPLICANT: ONO, YOICHI
APPLICANT: TOKIYOSHI, SACHIO
TITLE OF INVENTION: DOG-MOUSE HETEROHYBRIDOMA AND GENE
TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE
TITLE OF INVENTION: IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,981
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1488-106
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-646-981-16

Query Match 27.6%; Score 512; DB 2; Length 334;
Best Local Similarity 35.9%; Pred. No. 1.7e-41;
Matches 123; Conservative 60; Mismatches 122; Indels 38; Gaps 12;

QY 23 PTYVLFHSSCDPRGDHSTTQLCLVSGFSPAKVHTW----LVDCQEAENLFPYTTTRK 78
DB 5 PSVFPDLPSCG--STSGSTVALCLVSGYFPEPVVSMNSGSLTSG-----VHTFPD 55

QY 79 REGGQTPSLOSEVNTIQGQMSNTYTCYKH-----NSIFE--DSSRK 121
DB 56 LQSGGLVSLSNVTVPESRW--SSETPTONVAHASTKVDKVPKRENGKVPFPCCPC 114

QY 122 CABSNGVSAIYSRSPFP-LFIRKSPITTCVVDLAPSKGTNLTWSASGKPVNHS- 179
DB 115 PABMLGSPSVFTFPPEPKDTLLIARTPEVTCVVDLGEDEPVOISWF-VGKQMQTAK 173

QY 180 TRKEKQKNGTLTVTSTLPVGTWDWIEGETYQCRVTHPHLPALMRSTTKLPGKRLAPVY 239
DB 174 TORREBFGNTYVAVSLPIGHQDMLKQKFTCKVNNKALPSIEITISKARQAHQPSV 233

QY 240 YMLPSPER-TGTRTVTCLIRGFYSEISVQMLFNNEEDHTGHTTTPPOKDGTDPGF 298
DB 234 YVLPSPREKLSKNTVSLTCLIKDFFPPDIDVEQNSGQEPBSKRTTPQDLE--DGSY 291

QY 299 FLYSRMLVNSKIMEKGNLTVCRVYHALPGSRILESLHYSAG 341
DB 292 FLYSKLSYDKSQWQGDPTFCVAVHEALNNHT--QKSLSHSPG 333

RESULT 12
US-08-464-025A-1
Sequence 1, Application US/08464025A
Patent No. 5994514
GENERAL INFORMATION:
APPLICANT: Jarden et al.
TITLE OF INVENTION: IMMUNOGLOBULIN VARIANTS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,025A
FILING DATE: 05-Jun-1995
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Sueboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-464-025A-1

Query Match 27.4%; Score 508; DB 2; Length 119;
Best Local Similarity 88.9%; Pred. No. 8.7e-42;
Matches 104; Conservative 1; Mismatches 4; Indels 8; Gaps 4;

QY 124 DSNPRGVSAVLSRPSFDL-IFIRKSPITICLVVDLAPSKGVNLTWSRAS--GKPVNHS 179
DB 2 DSNPRGVSAVLSRPSFDLFIKSPITICLVVDLAPSKGVNLTWSRASXGKPVNHS 61

QY 180 TREEROR--NCTLTSTLPVGTDMTEGETYQCRVTHPHL-NRSTTKLPG 232
DB 62 TREERORXKXKSTLTSTLPVGTDMTEGETYQCRVTHPHLPRALXKRSSTTKSG 118

RESULT 13
US-08-646-981-17
Sequence 17, Application US/08646981
Patent No. 5852183
GENERAL INFORMATION:
APPLICANT: MAEDA, HIROAKI
APPLICANT: EDA, YASUYUKI
APPLICANT: KIMACHI, KAZUHIKO
APPLICANT: ONO, YOICHI
APPLICANT: TOKIYOSHI, SACHIO
TITLE OF INVENTION: DOG-MOUSE HETEROHYBRIDOMA AND GENE
TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE
TITLE OF INVENTION: IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,981
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1488-106
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-646-981-17

Query Match 27.0%; Score 501.5; DB 2; Length 331;
Best Local Similarity 36.3%; Pred. No. 1.7e-40;
Matches 122; Conservative 62; Mismatches 125; Indels 27; Gaps 12;

QY 23 PTYKLFHSSCDPRGDASTIQLCLVSGFSPAKVHTWLVQGEAENLPEYTTTRPKREG 82
DB 5 PSVPEPLAPSCG--STGSGIVTLACTVSGYFPEPVWSM-NSGSLTSGVHTFPEVLKSSG- 60

QY 83 QTFSLQSENVNITQGMSSNTVTCVHKNS-----FEQSSRKCDNSN-----RG 129
DB 61 -LISLSMTVTPSSR-LPSETFCNVVHPATNTKVDKPGVPSKSTCKLSPCEVPSLGG 118

QY 130 VSAVLSRPSFDL-IFIRKSPITICLVVDLAPSKGVNLTWSRASGKPVNHS-TREKOR 187
DB 119 PSVIFPPEPKDILIRITREVTVCVLDLREDPEVQISWF-VDGKEVHTAKTPREQQF 177

QY 188 NGULTVTSTLPVGRDMEGETYQCRVTHPHLPRALNRSTTKLPGKRLAPEVMTLPSPSE 247
DB 178 NSTYRVSVLPFIEHODLTGKEFKCRVNHIGLPSPIERTISKRGQHQGVVLPSPSK 237

QY 248 E--TGTRVTVCLIRGFYPSISVQWLFNNEBDHTGHTTRPOKHGTDPSFELYRML 305
DB 238 ELSSDVTVTLCIKDFPEIDVWQSNQPEPESKHTTARQDB--DGSYFLYSKLS 295

QY 306 VNSIKWKNLVTCRVVHEALPESRTLEKSLHYSAG 341
DB 296 VDKSRMEQDGFPCAWEHALQNHYT-DLSLHSPG 330

RESULT 14
US-08-788-800-12
Sequence 12, Application US/08788800
Patent No. 5914112
GENERAL INFORMATION:
APPLICANT: Bednar, Martin M.
APPLICANT: Thomas, G. Roger
APPLICANT: Gross, Cordell E.
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,800
FILING DATE: 22-Jan-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0987r1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-788-800-12

Query Match 26.5%; Score 492.5; DB 2; Length 450;
Best Local Similarity 36.5%; Pred. No. 2e-39;
Matches 118; Conservative 57; Mismatches 119; Indels 29; Gaps 11;

QY 35 RGDASHRTQLCLVSGSPAKVHTW---LVQGEAENLPEYTTTRPKREGGTFSLQSE 90

Db 140 RSTSESTALGCLVVDYFPEPVTVSWNSGALTSG---VHTFPAVL-----QSSGLYSLSV 192
 QY 91 VNITOGQWMSNTYTCHVKG---NGSIFEDSSRKCADSNP-----RGVSAYLSRPSPF 140
 Db 193 VVITSSNF-GTQYITCNVDHKPSNTKVDKVERKCCVCEPCBPAPVAPSVFLFPPPKX 251
 QY 141 D-LPIRKSPTITCLVVDLAPSKGTVNLWSPASGKPVNHSRKEKORNGTLTVTSTLPV 199
 Db 253 DTLMISRTPEVTCVVDVSHEDPEVOFNWYVDGMEVHNAKTYPREEQFNSTFRVSVLTV 311
 QY 200 GTRDWIEGTYOQRYTHPHLPALMRSTTKLPGRKLAPVYMLPPSPBE-TGTRTVTCL 258
 Db 312 VHODWLNKGEYKCKVSNKGLPAPIEKTSKTKQPREPOVYTLPPSRBEKTKNOVSLTCL 371
 QY 259 IRGFYPSSEISVQWLFNNEBDHGHHTTTPPOKHGTDPSFPLYSRMLVNSIWEKGNLTV 318
 Db 372 VKGFYPSDIAVEWESNGOPEN--NYKTPPMLD--SDGSFPLYSKLTVDKSRMOQGNVFS 427
 QY 319 CRVHEALPGSRRTLEKSLHYSAG 341
 Db 428 CSVHEALHNHT-OKSLSLSPG 449

RESULT 15
 US-07-934-373C-23
 ; Sequence 23, Application US/07934373C
 ; Patent No. 5821337

GENERAL INFORMATION:

APPLICANT: Paul J. Carter
 APPLICANT: Leonard G. Prestea
 TITLE OF INVENTION: Immunoglobulin Variants
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/934,373C
 FILING DATE: 21-Aug-1992
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/05126
 FILING DATE: 15-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/715272
 FILING DATE: 14-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P070992
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1994
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 469 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-07-934-373C-23

Query Match 26.5%; Score 492.5; DB 2; Length 469;
 Best Local Similarity 36.5%; Pred. No. 2.2e-39;
 Matches 118; Conservative 57; Mismatches 119; Indels 29; Gaps 11;

QY 35 RGDASTITQLCLVSGFSPAKVHTW----LVDOGAEANLFPYTTTPRKGEGQTFSLQSE 90

Db 159 RSTSESTALGCLVVDYFPEPVTVSWNSGALTSG---VHTFPAVL-----QSSGLYSLSV 211
 QY 91 VNITOGQWMSNTYTCHVKG---NGSIFEDSSRKCADSNP-----RGVSAYLSRPSPF 140
 Db 212 VVITSSNF-GTQYITCNVDHKPSNTKVDKVERKCCVCEPCBPAPVAPSVFLFPPPKX 270
 QY 141 D-LPIRKSPTITCLVVDLAPSKGTVNLWSPASGKPVNHSRKEKORNGTLTVTSTLPV 199
 Db 271 DTLMISRTPEVTCVVDVSHEDPEVOFNWYVDGMEVHNAKTYPREEQFNSTFRVSVLTV 330
 QY 200 GTRDWIEGTYOQRYTHPHLPALMRSTTKLPGRKLAPVYMLPPSPBE-TGTRTVTCL 258
 Db 331 VHODWLNKGEYKCKVSNKGLPAPIEKTSKTKQPREPOVYTLPPSRBEKTKNOVSLTCL 390
 QY 259 IRGFYPSSEISVQWLFNNEBDHGHHTTTPPOKHGTDPSFPLYSRMLVNSIWEKGNLTV 318
 Db 391 VKGFYPSDIAVEWESNGOPEN--NYKTPPMLD--SDGSFPLYSKLTVDKSRMOQGNVFS 446
 QY 319 CRVHEALPGSRRTLEKSLHYSAG 341
 Db 447 CSVHEALHNHT-OKSLSLSPG 468

Search completed: February 26, 2004, 12:04:43
 Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 11:59:57 : Search time 38 Seconds

(without alignments)
1900.379 Million cell updates/sec

Title: US-09-401-636-8

Perfect score: 1856
Sequence: 1 EPHHHHTLSPESGPVTI.....HEALPGRTLEKSLHYAGN 342

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 21153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1856	100.0	342	9	US-09-401-636-8
2	1856	100.0	342	14	US-10-176-664-8
3	1644.5	88.6	341	9	US-09-401-636-11
4	1644.5	88.6	341	14	US-10-176-664-11
5	1587.5	85.5	341	9	US-09-401-636-3
6	1587.5	85.5	341	14	US-10-176-664-3
7	1587.5	85.5	345	9	US-09-401-636-10
8	1587.5	85.5	345	14	US-10-176-664-10
9	1568.5	84.5	341	9	US-09-401-636-9
10	1568.5	84.5	341	14	US-10-176-664-9
11	1553.5	83.7	341	9	US-09-401-636-4
12	1553.5	83.7	341	14	US-10-176-664-4
13	1528.5	82.4	341	9	US-09-401-636-6
14	1528.5	82.4	341	14	US-10-176-664-6
15	1523.5	82.1	446	14	US-10-214-524-32

16	1519	81.8	342	9	US-09-401-636-5	Sequence 5, Appli
17	1519	81.8	342	14	US-10-176-664-5	Sequence 5, Appli
18	1285.5	69.3	427	14	US-10-214-524-36	Sequence 36, Appli
19	1050.5	56.6	343	9	US-09-401-636-7	Sequence 7, Appli
20	1050.5	56.6	343	14	US-10-176-664-7	Sequence 7, Appli
21	1045.5	56.3	569	10	US-09-847-208-7	Sequence 29, Appli
22	1044	56.2	527	14	US-10-214-524-29	Sequence 29, Appli
23	1038.5	56.0	320	10	US-09-847-208-6	Sequence 6, Appli
24	1038.5	56.0	323	9	US-09-949-375A-6	Sequence 6, Appli
25	1038.5	56.0	323	9	US-09-949-375A-6	Sequence 4, Appli
26	1038.5	56.0	323	9	US-09-949-375A-6	Sequence 6, Appli
27	1038.5	56.0	331	9	US-09-401-636-1	Sequence 1, Appli
28	1038.5	56.0	331	14	US-10-176-664-1	Sequence 1, Appli
29	1038.5	56.0	331	14	US-10-207-655-329	Sequence 329, App
30	1038.5	56.0	427	10	US-09-847-208-5	Sequence 5, Appli
31	1038.5	56.0	428	9	US-09-916-230-1	Sequence 1, Appli
32	1038.5	56.0	428	9	US-09-949-375A-1	Sequence 1, Appli
33	1038.5	56.0	428	13	US-10-047-542-60	Sequence 60, Appli
34	1038.5	56.0	574	13	US-10-047-542-45	Sequence 45, Appli
35	1038.5	56.0	574	14	US-10-214-524-37	Sequence 37, Appli
36	1038.5	56.0	574	14	US-10-050-962-176	Sequence 176, App
37	1038.5	56.0	574	14	US-10-050-962-176	Sequence 176, App
38	1038.5	56.0	592	14	US-10-207-655-334	Sequence 334, App
39	1036.5	55.8	330	9	US-09-949-375A-10	Sequence 10, Appli
40	1034.5	55.7	336	9	US-09-949-375A-8	Sequence 8, Appli
41	1034.5	55.7	441	9	US-09-949-375A-7	Sequence 7, Appli
42	1024.5	55.2	426	14	US-10-214-524-26	Sequence 26, Appli
43	996.5	53.7	347	14	US-10-152-190-13	Sequence 13, Appli
44	989	53.3	426	14	US-10-214-524-28	Sequence 28, Appli
45	978	52.7	496	14	US-10-214-524-25	Sequence 25, Appli

ALIGNMENTS

RESULT 1
US-09-401-636-8
Sequence 8, Application US/09401636
Patent No. US2001003843A1
GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10923/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 342
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-8

Query Match	100.0%	Score 1856;	DB 9;	Length 342;
Best Local Similarity	100.0%	Pred. No. 1.4e-146;		
Matches 342;	Conservative	0;	Mismatches 0;	Indels 0;
			Gaps 0;	
QY	1	EPHHHHHTLSPESGPVTIIPPTVYKLRHSSCDPRGDHSTIQLCLVSGSPAKVHTW	60	Sequence 5, Appli
DB	1	EPHHHHHTLSPESGPVTIIPPTVYKLRHSSCDPRGDHSTIQLCLVSGSPAKVHTW	60	Sequence 36, Appli
QY	61	LVDDGAEALFFYTRPRKRGQTSLQSEVNIITGOMSSNTTYCHYKXNSITFEDSR	120	Sequence 7, Appli
DB	61	LVDDGAEALFFYTRPRKRGQTSLQSEVNIITGOMSSNTTYCHYKXNSITFEDSR	120	Sequence 29, Appli
QY	121	KCADSNPRVSAVYLSRSPFDLFIKRSPTITCLVVDLAPSKQTVMLTWSRSGKPVNST	180	Sequence 6, Appli
DB	121	KCADSNPRVSAVYLSRSPFDLFIKRSPTITCLVVDLAPSKQTVMLTWSRSGKPVNST	180	Sequence 4, Appli
QY	121	KCADSNPRVSAVYLSRSPFDLFIKRSPTITCLVVDLAPSKQTVMLTWSRSGKPVNST	180	Sequence 6, Appli
DB	121	KCADSNPRVSAVYLSRSPFDLFIKRSPTITCLVVDLAPSKQTVMLTWSRSGKPVNST	180	Sequence 13, Appli

QY 181 RKEKQNGTLVTVSTLPVGRDMIGETVQCRVTHPHLPALMRSTTLPGKRLAPEVY 240
DB 181 RKEKQNGTLVTVSTLPVGRDMIGETVQCRVTHPHLPALMRSTTLPGKRLAPEVY 240
QY 241 MLPSPSEETGTRTVCLIRGFYPSSEISVQWLFNNEEDHTGHTTTRPOKHGTDPSPFL 300
DB 241 MLPSPSEETGTRTVCLIRGFYPSSEISVQWLFNNEEDHTGHTTTRPOKHGTDPSPFL 300
QY 301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRITLKSILHYSAGN 342
DB 301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRITLKSILHYSAGN 342

RESULT 2
US-10-176-664-8
; Sequence 8, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 342
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-8

Query Match 100.0%; Score 1856; DB 14; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.4e-146;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDASTTQLCLVSGFSPAKVHTW 60
DB 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDASTTQLCLVSGFSPAKVHTW 60
QY 61 LVDCQEAENLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCVHNGSIFEDSSR 120
DB 61 LVDCQEAENLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCVHNGSIFEDSSR 120
QY 121 KCADSNPRGVSAVLSRSPFDLFIKRSPTITCLVVDLADSKGTVNLWRSAGKPVNHS 180
DB 121 KCADSNPRGVSAVLSRSPFDLFIKRSPTITCLVVDLADSKGTVNLWRSAGKPVNHS 180
QY 181 RKEKQNGTLVTVSTLPVGRDMIGETVQCRVTHPHLPALMRSTTLPGKRLAPEVY 240
DB 181 RKEKQNGTLVTVSTLPVGRDMIGETVQCRVTHPHLPALMRSTTLPGKRLAPEVY 240
QY 241 MLPSPSEETGTRTVCLIRGFYPSSEISVQWLFNNEEDHTGHTTTRPOKHGTDPSPFL 300
DB 241 MLPSPSEETGTRTVCLIRGFYPSSEISVQWLFNNEEDHTGHTTTRPOKHGTDPSPFL 300
QY 301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRITLKSILHYSAGN 342
DB 301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRITLKSILHYSAGN 342

RESULT 3
US-09-401-636-11
; Sequence 11, Application US/09401636
; Patent No. US2001003843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES

FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-11

Query Match 88.6%; Score 1644.5; DB 9; Length 341;
Best Local Similarity 88.0%; Pred. No. 6.2e-129;
Matches 301; Conservative 17; Mismatches 23; Indels 1; Gaps 1;

QY 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDASTTQLCLVSGFSPAKVHTW 60
DB 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDASTTQLCLVSGFSPAKVHTW 60
QY 61 LVDCQEAENLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCVHNGSIFEDSSR 120
DB 61 LVDCQEAENLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCVHNGSIFEDSSR 120
QY 121 KCADSNPRGVSAVLSRSPFDLFIKRSPTITCLVVDLADSKGTVNLWRSAGKPVNHS 180
DB 121 KCADSNPRGVSAVLSRSPFDLFIKRSPTITCLVVDLADSKGTVNLWRSAGKPVNHS 180
QY 181 RKEKQNGTLVTVSTLPVGRDMIGETVQCRVTHPHLPALMRSTTLPGKRLAPEVY 240
DB 181 RKEKQNGTLVTVSTLPVGRDMIGETVQCRVTHPHLPALMRSTTLPGKRLAPEVY 240
QY 241 MLPSPSEETGTRTVCLIRGFYPSSEISVQWLFNNEEDHTGHTTTRPOKHGTDPSPFL 300
DB 241 MLPSPSEETGTRTVCLIRGFYPSSEISVQWLFNNEEDHTGHTTTRPOKHGTDPSPFL 300
QY 301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRITLKSILHYSAGN 342
DB 301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRITLKSILHYSAGN 342

RESULT 4
US-10-176-664-11
; Sequence 11, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-11

Query Match 88.6%; Score 1644.5; DB 14; Length 341;
Best Local Similarity 88.0%; Pred. No. 6.2e-129;
Matches 301; Conservative 17; Mismatches 23; Indels 1; Gaps 1;

QY 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDASTTQLCLVSGFSPAKVHTW 60

```

Db      1 EFHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60
Qy      61 LVDQGEAENLPFYTRPRREGGQTFSLQSEVNITQOGWMSNTYTCVKENGSIFFEDSSR 120
Db      61 LVDQGEAENLPFYTRPRREGGQTFSLQSEVNITQOGWMSNTYTCVKENGSIFFEDSSR 120
Qy      121 KCADSNPRGVSAVYLSRPSFPDLFIRKSPITTCVVDLAPSKGTYNLTWSASGKPVNHS 180
Db      121 KCSDSDPRGVTSYLSRPSFDLLVHKAPKITCLVVDLAMEG-MULTWYKESKEPVNPG 179
Qy      181 RKEEKORNGTLVTSTLPVGRDMEIGETTYQCRVTHPHLPALMRSTTKLPGKRLAPEVY 240
Db      180 LNKDHFVGTITVTSTLPVNTNDWIEGETTYQCRVTHPHLPDVIYSIAKIPGKRLAPEVY 239
Qy      241 MLPSPEBTGTRVTCIRGFPSEISVQWLFNNEBDHGHHTTTPQKHGTDPSFFL 300
Db      240 MLPSPEBTGTRVTCIRGFPSEISVQWLFNNEBDHGHHTTTPQKHGTDPSFFL 299
Qy      301 YSRMLVNSIWEKGNLVTCRVVHEALPGSRITLKSILHYSAGN 342
Db      300 YSRMLVNSIWEKGNLVTCRVVHEALPGSRITLKSILHYSAGN 341

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RESULT 5 US-09-401-636-3

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; Sequence 3, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-3

```

```

Query Match      85.5%; Score 1587.5; DB 9; Length 341;
Best Local Similarity 85.4%; Pred. No. 3.5e-124;
Matches 292; Conservative 21; Mismatches 28; Indels 1; Gaps 1;

Qy      1 EFHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60
Db      1 EFHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60
Qy      61 LVDQGEAENLPFYTRPRREGGQTFSLQSEVNITQOGWMSNTYTCVKENGSIFFEDSSR 120
Db      61 LVDQGEAENLPFYTRPRREGGQTFSLQSEVNITQOGWMSNTYTCVKENGSIFFEDSSR 120
Qy      121 KCADSNPRGVSAVYLSRPSFPDLFIRKSPITTCVVDLAPSKGTYNLTWSASGKPVNHS 180
Db      121 KCSDSDPRGVTSYLSRPSFDLLVHKAPKITCLVVDLAMEG-SAEVNKYVWSRESGKPVNPS 179
Qy      181 RKEEKORNGTLVTSTLPVGRDMEIGETTYQCRVTHPHLPALMRSTTKLPGKRLAPEVY 240
Db      180 LVVKEQVNGITVTSHLPVNTNDWIEGDTYTCRLESDDMVPLIRITSKAPGKRLAPEVY 239
Qy      241 MLPSPEBTGTRVTCIRGFPSEISVQWLFNNEBDHGHHTTTPQKHGTDPSFFL 300
Db      240 MLPSPEBTGTRVTCIRGFPSEISVQWLFNNEBDHGHHTTTPQKHGTDPSFFL 299
Qy      301 YSRMLVNSIWEKGNLVTCRVVHEALPGSRITLKSILHYSAGN 342
Db      300 YSRMLVNSIWEKGNLVTCRVVHEALPGSRITLKSILHYSAGN 341

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RESULT 6
US-10-176-664-3
; Sequence 3, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-3

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Query Match      85.5%; Score 1587.5; DB 14; Length 341;
Best Local Similarity 85.4%; Pred. No. 3.5e-124;
Matches 292; Conservative 21; Mismatches 28; Indels 1; Gaps 1;

Qy      1 EFHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60
Db      1 EFHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60
Qy      61 LVDQGEAENLPFYTRPRREGGQTFSLQSEVNITQOGWMSNTYTCVKENGSIFFEDSSR 120
Db      61 LVDQGEAENLPFYTRPRREGGQTFSLQSEVNITQOGWMSNTYTCVKENGSIFFEDSSR 120
Qy      121 KCADSNPRGVSAVYLSRPSFPDLFIRKSPITTCVVDLAPSKGTYNLTWSASGKPVNHS 180
Db      121 KCSDSDPRGVTSYLSRPSFDLLVHKAPKITCLVVDLAMEG-SAEVNKYVWSRESGKPVNPS 179
Qy      181 RKEEKORNGTLVTSTLPVGRDMEIGETTYQCRVTHPHLPALMRSTTKLPGKRLAPEVY 240
Db      180 LVVKEQVNGITVTSHLPVNTNDWIEGDTYTCRLESDDMVPLIRITSKAPGKRLAPEVY 239
Qy      241 MLPSPEBTGTRVTCIRGFPSEISVQWLFNNEBDHGHHTTTPQKHGTDPSFFL 300
Db      240 MLPSPEBTGTRVTCIRGFPSEISVQWLFNNEBDHGHHTTTPQKHGTDPSFFL 299
Qy      301 YSRMLVNSIWEKGNLVTCRVVHEALPGSRITLKSILHYSAGN 342
Db      300 YSRMLVNSIWEKGNLVTCRVVHEALPGSRITLKSILHYSAGN 341

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RESULT 7
US-09-401-636-10
; Sequence 10, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 345
; TYPE: PR1
; ORGANISM: Artificial Sequence

```

FEATURE:
OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-10

Query Match 85.5%; Score 1587.5; DB 9; Length 345;
Best Local Similarity 84.7%; Pred. No. 3.5e-124;
Matches 298; Conservative 14; Mismatches 23; Indels 17; Gaps 4;

QY 1 EFNHHHHTSLPESGPTVITPTVTLFHSSCDPRDASTIQLCLVSGSPAKVHTW 60
DB 1 EFNHHHHTSLPESGPTVITPTVTLFHSSCDPRDASTIQLCLVSGSPAKVHTW 60
QY 61 LVDSQAEMLFPYTRPKRGQGFSLQSEVNITQGMMSNTYTCHVGNISIFEDSSR 120
DB 61 LVDSQAEMLFPYTRPKRGQGFSLQSEVNITQGMMSNTYTCHVGNISIFEDSSR 120
QY 121 KC-ADSNPRGVSAVLSRSPFDLFIKSPITICLVVDLAPSGVTWLTMSRAS----- 172
DB 121 RCTAESBPRGVSAVLSRSPFDLFIKSPITICLVVDLAPSGVTWLTMSRAS----- 172
QY 173 --GKPVNSTRKEKORNGTLVTVSTLPGTRDMIEGETYQCRVTHPHLPALMRSTTKL 230
DB 180 PRGPV-----IKPQNGTFSATSTLPVNSDMIGETYYCNVTHPDLPKILRSISKL 233
QY 231 PGKRLAPEVYMLPPSPETGTRTVCLIRGFPSISVQWLFNNEEDHTGHTTTRPOK 290
DB 234 PGKRLAPEVYMLPPSPETGTRTVCLIRGFPSISVQWLFNNEEDHTGHTTTRPOK 293
QY 291 DHGTDSPFLYSRMLVNSKIWEKGNLVTCRVVHEALPGSRITLKSLSHYSAGN 342
DB 294 DHGTDSPFLYSRMLVNSKIWEKGNLVTCRVVHEALPGSRITLKSLSHYSAGN 345

RESULT 8
US-10-176-664-10
Sequence 10, Application US/10176664
Publication No. US20030031663A1
GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/10/176,664
CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: US/09/401,636
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 345
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-10

Query Match 85.5%; Score 1587.5; DB 14; Length 345;
Best Local Similarity 84.7%; Pred. No. 3.5e-124;
Matches 298; Conservative 14; Mismatches 23; Indels 17; Gaps 4;

QY 1 EFNHHHHTSLPESGPTVITPTVTLFHSSCDPRDASTIQLCLVSGSPAKVHTW 60
DB 1 EFNHHHHTSLPESGPTVITPTVTLFHSSCDPRDASTIQLCLVSGSPAKVHTW 60
QY 61 LVDSQAEMLFPYTRPKRGQGFSLQSEVNITQGMMSNTYTCHVGNISIFEDSSR 120
DB 61 LVDSQAEMLFPYTRPKRGQGFSLQSEVNITQGMMSNTYTCHVGNISIFEDSSR 120
QY 121 KC-ADSNPRGVSAVLSRSPFDLFIKSPITICLVVDLAPSGVTWLTMSRAS----- 172
DB 121 RCTAESBPRGVSAVLSRSPFDLFIKSPITICLVVDLAPSGVTWLTMSRAS----- 172

QY 173 --GKPVNSTRKEKORNGTLVTVSTLPGTRDMIEGETYQCRVTHPHLPALMRSTTKL 230
DB 180 PRGPV-----IKPQNGTFSATSTLPVNSDMIGETYYCNVTHPDLPKILRSISKL 233
QY 231 PGKRLAPEVYMLPPSPETGTRTVCLIRGFPSISVQWLFNNEEDHTGHTTTRPOK 290
DB 234 PGKRLAPEVYMLPPSPETGTRTVCLIRGFPSISVQWLFNNEEDHTGHTTTRPOK 293
QY 291 DHGTDSPFLYSRMLVNSKIWEKGNLVTCRVVHEALPGSRITLKSLSHYSAGN 342
DB 294 DHGTDSPFLYSRMLVNSKIWEKGNLVTCRVVHEALPGSRITLKSLSHYSAGN 345

RESULT 9
US-09-401-636-9
Sequence 9, Application US/09401636
Patent No. US20010038843A1
GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 341
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-9

Query Match 84.5%; Score 1568.5; DB 9; Length 341;
Best Local Similarity 83.3%; Pred. No. 1.3e-122;
Matches 285; Conservative 20; Mismatches 36; Indels 1; Gaps 1;

QY 1 EFNHHHHTSLPESGPTVITPTVTLFHSSCDPRDASTIQLCLVSGSPAKVHTW 60
DB 1 EFNHHHHTSLPESGPTVITPTVTLFHSSCDPRDASTIQLCLVSGSPAKVHTW 60
QY 61 LVDSQAEMLFPYTRPKRGQGFSLQSEVNITQGMMSNTYTCHVGNISIFEDSSR 120
DB 61 LVDSQAEMLFPYTRPKRGQGFSLQSEVNITQGMMSNTYTCHVGNISIFEDSSR 120
QY 121 KCADSNPRGVSAVLSRSPFDLFIKSPITICLVVDLAPSGVTWLTMSRASGKPVNHT 180
DB 121 RCDSDPRGVITLIPSPPLDLYENGTGPKLTVLVL-SEENITVWREKRSIGSAS 179
QY 181 RKEKORNGTLVTVSTLPGTRDMIEGETYQCRVTHPHLPALMRSTTKLPGKRLAPEVY 240
DB 180 QRETKHNAATSTISLIPVDAKMIGEGQCKVDHPHPKPIVRSITLPGKRLAPEVY 239
QY 241 MLPPSPETGTRTVCLIRGFPSISVQWLFNNEEDHTGHTTTRPOKDHGTDSPFL 300
DB 240 MLPPSPETGTRTVCLIRGFPSISVQWLFNNEEDHTGHTTTRPOKDHGTDSPFL 299
QY 301 YSRMLVNSKIWEKGNLVTCRVVHEALPGSRITLKSLSHYSAGN 342
DB 300 YSRMLVNSKIWEKGNLVTCRVVHEALPGSRITLKSLSHYSAGN 341

RESULT 10
US-10-176-664-9
Sequence 9, Application US/10176664
Publication No. US20030031663A1
GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/10/176,664

CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: US/09/401,636
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 341
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-9

Query Match 84.5%; Score 1568.5; DB 14; Length 341;
Best Local Similarity 83.3%; Pred. No. 1,3e-122;
Matches 285; Conservative 20; Mismatches 36; Indels 1; Gaps 1;

QY 1 EFHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60
DB 1 EFHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60
QY 61 LVDGGAENLFPYTRPRKGGQTSLOSEVNITOGQWMSNTYTCVKNKNGSIFEDSSR 120
DB 61 LVDGGAENLFPYTRPRKGGQTSLOSEVNITOGQWMSNTYTCVKNKNGSIFEDSSR 120
QY 121 KCADSNPRGSAVLSRSPFDLFIKSPITICLVLDAPSCKTVNLWRSRAGKPVNHS 180
DB 121 KCADSNPRGSAVLSRSPFDLFIKSPITICLVLDAPSCKTVNLWRSRAGKPVNHS 180
QY 121 RCDSDPRGVITVTLIPSPDLVYENGTPKLCVLDL-ESEENITVWVRKKSIGSAS 179
DB 121 RCDSDPRGVITVTLIPSPDLVYENGTPKLCVLDL-ESEENITVWVRKKSIGSAS 179
QY 181 RKEKORNGTLVTSTLPVGRDWTGEGTYQCRVTHPHLPALMRSTTKLPKRLAPEVY 240
DB 181 RKEKORNGTLVTSTLPVGRDWTGEGTYQCRVTHPHLPALMRSTTKLPKRLAPEVY 240
QY 180 ORSTKHNAHTSITSLIPVDADKWIIEGEGYQCRVDHPHPKPIVASITKLPKRLAPEVY 239
DB 180 ORSTKHNAHTSITSLIPVDADKWIIEGEGYQCRVDHPHPKPIVASITKLPKRLAPEVY 239
QY 241 MLPSPPEETGTRTYTCLIRGFYPSISVQWLFNNEEDHTGHHTTRPOKHGTDPSFPL 300
DB 241 MLPSPPEETGTRTYTCLIRGFYPSISVQWLFNNEEDHTGHHTTRPOKHGTDPSFPL 300
QY 301 YSRMLVNXSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
DB 301 YSRMLVNXSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
QY 300 YSRMLVNXSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341
DB 300 YSRMLVNXSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341

RESULT 11

US-09-401-636-4
Sequence 4, Application US/09401636
Patent No. US20010038843A1
GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 341
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-4

Query Match 83.7%; Score 1553.5; DB 9; Length 341;
Best Local Similarity 82.7%; Pred. No. 2.4e-121;
Matches 283; Conservative 21; Mismatches 37; Indels 1; Gaps 1;
QY 1 EFHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60
DB 1 EFHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60

QY 61 LVDGGAENLFPYTRPRKGGQTSLOSEVNITOGQWMSNTYTCVKNKNGSIFEDSSR 120
DB 61 LVDGGAENLFPYTRPRKGGQTSLOSEVNITOGQWMSNTYTCVKNKNGSIFEDSSR 120
QY 121 KCADSNPRGSAVLSRSPFDLFIKSPITICLVLDAPSCKTVNLWRSRAGKPVNHS 180
DB 121 KCADSNPRGSAVLSRSPFDLFIKSPITICLVLDAPSCKTVNLWRSRAGKPVNHS 180
QY 121 RCDSDPRGVITVTLIPSPDLVYENGTPKLCVLDL-ESEENITVWVRKKSIGSAS 179
DB 121 RCDSDPRGVITVTLIPSPDLVYENGTPKLCVLDL-ESEENITVWVRKKSIGSAS 179
QY 181 RKEKORNGTLVTSTLPVGRDWTGEGTYQCRVTHPHLPALMRSTTKLPKRLAPEVY 240
DB 181 RKEKORNGTLVTSTLPVGRDWTGEGTYQCRVTHPHLPALMRSTTKLPKRLAPEVY 240
QY 180 ORSTKHNAHTSITSLIPVDADKWIIEGEGYQCRVDHPHPKPIVASITKLPKRLAPEVY 239
DB 180 ORSTKHNAHTSITSLIPVDADKWIIEGEGYQCRVDHPHPKPIVASITKLPKRLAPEVY 239
QY 241 MLPSPPEETGTRTYTCLIRGFYPSISVQWLFNNEEDHTGHHTTRPOKHGTDPSFPL 300
DB 241 MLPSPPEETGTRTYTCLIRGFYPSISVQWLFNNEEDHTGHHTTRPOKHGTDPSFPL 300
QY 301 YSRMLVNXSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
DB 301 YSRMLVNXSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341

RESULT 12

US-10-176-664-4
Sequence 4, Application US/10176664
Publication No. US20030031663A1
GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/10/176,664
CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: US/09/401,636
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 341
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-4

Query Match 83.7%; Score 1553.5; DB 14; Length 341;
Best Local Similarity 82.7%; Pred. No. 2.4e-121;
Matches 283; Conservative 21; Mismatches 37; Indels 1; Gaps 1;

QY 1 EFHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60
DB 1 EFHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60
QY 61 LVDGGAENLFPYTRPRKGGQTSLOSEVNITOGQWMSNTYTCVKNKNGSIFEDSSR 120
DB 61 LVDGGAENLFPYTRPRKGGQTSLOSEVNITOGQWMSNTYTCVKNKNGSIFEDSSR 120
QY 121 KCADSNPRGSAVLSRSPFDLFIKSPITICLVLDAPSCKTVNLWRSRAGKPVNHS 180
DB 121 KCADSNPRGSAVLSRSPFDLFIKSPITICLVLDAPSCKTVNLWRSRAGKPVNHS 180
QY 121 RCDSDPRGVITVTLIPSPDLVYENGTPKLCVLDL-ESEENITVWVRKKSIGSAS 179
DB 121 RCDSDPRGVITVTLIPSPDLVYENGTPKLCVLDL-ESEENITVWVRKKSIGSAS 179
QY 181 RKEKORNGTLVTSTLPVGRDWTGEGTYQCRVTHPHLPALMRSTTKLPKRLAPEVY 240
DB 181 RKEKORNGTLVTSTLPVGRDWTGEGTYQCRVTHPHLPALMRSTTKLPKRLAPEVY 240
QY 180 ORSTKHNAHTSITSLIPVDADKWIIEGEGYQCRVDHPHPKPIVASITKLPKRLAPEVY 239
DB 180 ORSTKHNAHTSITSLIPVDADKWIIEGEGYQCRVDHPHPKPIVASITKLPKRLAPEVY 239
QY 241 MLPSPPEETGTRTYTCLIRGFYPSISVQWLFNNEEDHTGHHTTRPOKHGTDPSFPL 300
DB 241 MLPSPPEETGTRTYTCLIRGFYPSISVQWLFNNEEDHTGHHTTRPOKHGTDPSFPL 300
QY 301 YSRMLVNXSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
DB 301 YSRMLVNXSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341

```

RESULT 13
US-09-401-636-6
; Sequence 6, Application US/09401636
; Patent No. US20010038643A1
; GENERAL INFORMATION:
; APPLICANT: Heliman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-6

```

```

Query Match      82.4%; Score 1528.5; DB 9; Length 341;
Best Local Similarity 83.0%; Pred. No. 2,9e-119;
Matches 284; Conservative 14; Mismatches 43; Indels 1; Gaps 1;

```

```

QY 1 EHHHHHHHTLSLPESGPTIIPTTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHYTM 60
DB 1 EHHHHHHHTLSLPESGPTIIPTTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHYTM 60
QY 61 LVDCGEAENLFPYTPPKRGGQTFSLQSEVNITQOGWMSNTYTCVKNKNGSIFEDSSR 120
DB 61 LVDCGEAENLFPYTPPKRGGQTFSLQSEVNITQOGWMSNTYTCVKNKNGSIFEDSSR 120
QY 121 KCADSNPRGSAVLSRSPFDLFRKSPFTTICLVLDLAPSKGTNLTWSRASGKPVNHST 180
DB 121 KCADSNPRGSAVLSRSPFDLFRKSPFTTICLVLDLAPSKGTNLTWSRASGKPVNHST 180
QY 121 RCPDHEPRGVTITLIPSPDLVYQNGAPKLTCLVLDLSEK-NVNTVMQEKTSVNASQ 179
DB 121 RCPDHEPRGVTITLIPSPDLVYQNGAPKLTCLVLDLSEK-NVNTVMQEKTSVNASQ 179
QY 181 RKEBKQNGTLVTSITLIPVAKDMIGYQCIVDHPDKPIVRSITLPGKRLAPEVY 240
DB 181 RKEBKQNGTLVTSITLIPVAKDMIGYQCIVDHPDKPIVRSITLPGKRLAPEVY 240
QY 241 MLPSPSETGTRTTCVCLIRGFYPSISYQWLFNNEEDHTGHTTTRPOKHGTDPSPFL 300
DB 241 MLPSPSETGTRTTCVCLIRGFYPSISYQWLFNNEEDHTGHTTTRPOKHGTDPSPFL 300
QY 240 MLPSPSETGTRTTCVCLIRGFYPSISYQWLFNNEEDHTGHTTTRPOKHGTDPSPFL 299
DB 240 MLPSPSETGTRTTCVCLIRGFYPSISYQWLFNNEEDHTGHTTTRPOKHGTDPSPFL 299
QY 301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRITLSEKSLHYAGN 342
DB 301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRITLSEKSLHYAGN 342

```

```

RESULT 14
US-10-176-664-6
; Sequence 6, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Heliman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-6

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Query Match      82.4%; Score 1528.5; DB 14; Length 446;
Best Local Similarity 83.0%; Pred. No. 1.1e-118;
Matches 283; Conservative 21; Mismatches 29; Indels 1; Gaps 1;

```

```

QY 1 EHHHHHHHTLSLPESGPTIIPTTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHYTM 60
DB 1 EHHHHHHHTLSLPESGPTIIPTTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHYTM 60
QY 61 LVDCGEAENLFPYTPPKRGGQTFSLQSEVNITQOGWMSNTYTCVKNKNGSIFEDSSR 120
DB 61 LVDCGEAENLFPYTPPKRGGQTFSLQSEVNITQOGWMSNTYTCVKNKNGSIFEDSSR 120
QY 121 KCADSNPRGSAVLSRSPFDLFRKSPFTTICLVLDLAPSKGTNLTWSRASGKPVNHST 180
DB 121 RCPDHEPRGVTITLIPSPDLVYQNGAPKLTCLVLDLSEK-NVNTVMQEKTSVNASQ 179
QY 181 RKEBKQNGTLVTSITLIPVAKDMIGYQCIVDHPDKPIVRSITLPGKRLAPEVY 240
DB 181 RKEBKQNGTLVTSITLIPVAKDMIGYQCIVDHPDKPIVRSITLPGKRLAPEVY 240
QY 241 MLPSPSETGTRTTCVCLIRGFYPSISYQWLFNNEEDHTGHTTTRPOKHGTDPSPFL 300
DB 240 MLPSPSETGTRTTCVCLIRGFYPSISYQWLFNNEEDHTGHTTTRPOKHGTDPSPFL 299
QY 301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRITLSEKSLHYAGN 342
DB 301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRITLSEKSLHYAGN 342

```

```

RESULT 15
US-10-214-524-32
; Sequence 32, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swey-Shen Alex
; APPLICANT: Chen, Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent version 3.1
; SEQ ID NO 32
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Opossum (Monodelphis domestica)
US-10-214-524-32

```

```

Query Match      82.1%; Score 1523.5; DB 14; Length 446;
Best Local Similarity 84.7%; Pred. No. 1.1e-118;
Matches 283; Conservative 21; Mismatches 29; Indels 1; Gaps 1;

```

```

QY 9 TLSLPESGPTIIPTTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHYTM 68
DB 114 TLSLPESGPTIIPTTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHYTM 68
QY 69 MLPSPSETGTRTTCVCLIRGFYPSISYQWLFNNEEDHTGHTTTRPOKHGTDPSPFL 128
DB 174 MLPSPSETGTRTTCVCLIRGFYPSISYQWLFNNEEDHTGHTTTRPOKHGTDPSPFL 128
QY 129 GSAVLSRSPFDLFRKSPFTTICLVLDLAPSKGTNLTWSRASGKPVNHST 188
DB 234 GSAVLSRSPFDLFRKSPFTTICLVLDLAPSKGTNLTWSRASGKPVNHST 188
QY 234 GSAVLSRSPFDLFRKSPFTTICLVLDLAPSKGTNLTWSRASGKPVNHST 188
DB 189 GSAVLSRSPFDLFRKSPFTTICLVLDLAPSKGTNLTWSRASGKPVNHST 188

```

Db	233	GFITVTSHPVNTDWMIEGDIYTCRLSPDMVPLIRITISKAPGKRLAPEVYMLPPSPPEE	352
Qy	249	TGTRTVTCLIRGFYPSISVOMLPNNEDHTGHTTTRPOKHGTDPSPFLYSRMLVNK	308
Db	353	TGTRTVTCLIRGFYPSISVOMLPNNEDHTGHTTTRPOKHGTDPSPFLYSRMLVNK	412
Qy	309	SIMEKGNLVTCEVVEALPGSRTLEKSLHYSAGN	342
Db	413	SIMEKGNLVTCEVVEALPGSRTLEKSLHYSAGN	446

Search completed: February 26, 2004, 12:05:55
 Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 11:42:41; Search time 59 Seconds

(without alignments)
1637.818 Million cell updates/sec

Title: US-09-401-636-8
Perfect score: 1856
Sequence: 1 EFHHHHHTTSLPESGPVTI.....HEALPGSRTLEKSLHYSGN 342

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_28Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003s:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1856	100.0	342	3	AAB06205 Immunogen
2	1644.5	88.6	341	3	AAB06208 Immunogen
3	1587.5	85.5	345	3	AAB06207 Immunogen
4	1584.5	85.4	341	3	AAB03644 Opossum I
5	1568.5	84.5	341	3	AAB06206 Opossum I
6	1523.5	82.1	446	6	ABP96587 Immunogen
7	1392.5	75.0	341	3	AAB06202 Immunogen
8	1375	74.1	342	6	AAB06201 Immunogen
9	1285.5	69.3	427	6	ABP96591 Brushtail
10	1045.5	56.3	569	6	ABP96591 GE2 fusio
11	1044	56.2	577	6	ABP96584 Duckbill
12	1038.5	56.0	320	6	AAB019667 Human IGE
13	1038.5	56.0	323	5	AAB080286 Human IGE
14	1038.5	56.0	323	5	AAB080285 Human IGE
15	1038.5	56.0	323	5	AAB080284 Human IGE
16	1038.5	56.0	324	2	AAB80359 Fc(eps)llo
17	1038.5	56.0	325	2	AAB75225 Human IGE
18	1038.5	56.0	325	2	AAB77241 Human IGE
19	1038.5	56.0	331	7	AAB03642 Human IGE
20	1038.5	56.0	331	7	ABD25768 Binding d
21	1038.5	56.0	367	1	AAB80291 Interleuk
22	1038.5	56.0	427	6	AAB47863 Human IGE
23	1038.5	56.0	428	5	AAB080283 Human IGE
24	1038.5	56.0	428	5	AAB50940 Human IGE
25	1038.5	56.0	428	5	AAB50940 Human IGE

26	1038.5	56.0	428	6	AAB35113 Human imm
27	1038.5	56.0	428	7	ADD48440 Human Pro
28	1038.5	56.0	574	5	ABG94250 Human IGE
29	1038.5	56.0	574	5	ABG80562 Human IGE
30	1038.5	56.0	574	6	ABP96592 Human IGE
31	1038.5	56.0	592	7	ADD25773 Binding d
32	1036.5	55.8	330	5	AAB80289 Human IGE
33	1035.5	55.8	325	3	AAB79994 Human imm
34	1034.5	55.7	431	5	AAB80287 Human IGE
35	1034.5	55.7	441	5	AAB80287 Human IGE
36	1030.5	55.5	493	1	AAP40065 Sequence
37	1024.5	55.2	426	6	ABP96581 Chimpanze
38	1019.5	54.9	315	2	AAB85582 Fc(eps)llo
39	1019.5	54.9	325	2	AAB83582 CH2 to CH
40	1010.5	54.4	425	6	AAB35114 Human imm
41	1002.5	54.0	428	2	AAB42950 Human imm
42	996.5	53.7	347	6	ABG74784 Human CH2
43	992.5	53.5	343	3	AAB06204 Placypus
44	989	53.3	426	6	ABP96583 Dog IGE h
45	978	52.7	496	6	ABP96580 Cat IGE h

ALIGNMENTS

RESULT 1
AAB06205
ID AAB06205 standard; protein; 342 AA.

AC AAB06205;
XX
XX
XX 12-SEP-2003 (revised)
DT 22-NOV-2000 (first entry)
XX
XX
DE Immunogenic peptide consisting of opossum CH2, human CH3 and opossum CH4.
XX
XX Human; opossum; immunoglobulin E; IGE; vaccination; infection; allergy;
KW acthma; eczema; immunogenic peptide.
XX
XX Didelphis virginiana.
OS Homo sapiens.
OS Chimeric.
XX
XX WO200025722-A2.
XX
XX PD 11-MAY-2000.
XX
XX 21-OCT-1999; 99WO-SE001896.
XX
XX 02-NOV-1998; 98US-0106652P.
PR 22-SEP-1999; 99US-00401636.
XX
XX (RESE-) RESISTENTIA PHARM AB.
XX
XX PI Helman LT;
XX
XX WPI; 2000-365342/31.
XX
XX Immunogenic polypeptides useful for preventing the harmful effects of
PT immunoglobulin E in mammals.
XX
XX
PS Disclosure; Fig 2; 50pp; English.
XX
XX The present sequence is an immunogenic peptide consisting of the heavy
CC chain constant regions 2 and 4 of the opossum IGE and the heavy chain
CC constant region 3 from the human. It was shown to cause a stronger
CC polyclonal anti-self IGE response than peptides consisting of the same
CC regions from one mammal. Immunogenic peptides, particularly those
CC consisting of different heavy chain constant regions, can be used for
CC vaccination in humans, against bacterial and viral infections and
CC allergies, such as asthma, fur, pollen and food allergies and eczema.
XX (Updated on 12-SEP-2003 to standardise OS field)

SQ Sequence 342 AA;
 Query Match 100.0%; Score 1856; DB 3; Length 342;
 Best Local Similarity 100.0%; Pred. No. 3.8e-146;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPHHHHHHTLSLPSGSPVITIIPTVTLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60
 DB 1 EPHHHHHHTLSLPSGSPVITIIPTVTLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60
 QY 61 LVVGOBAENLFPTTPKREGGOTFSLQSEVNITOGQMSNTYTCVHNGSIFEDSSR 120
 DB 61 LVVGOBAENLFPTTPKREGGOTFSLQSEVNITOGQMSNTYTCVHNGSIFEDSSR 120
 QY 121 KCADSNPRGVSAVLSRSPSPDLFIRKSPITTCIVDLAPSKGTNLTWSRAGKPVNHS 180
 DB 121 KCADSNPRGVSAVLSRSPSPDLFIRKSPITTCIVDLAPSKGTNLTWSRAGKPVNHS 180
 QY 181 RKEKQRNGTLVTSSTLPVGTDRWINGETVQCRVTHPHLPALMRSTTKLPKRLAPEVY 240
 DB 181 RKEKQRNGTLVTSSTLPVGTDRWINGETVQCRVTHPHLPALMRSTTKLPKRLAPEVY 240
 QY 241 MLPSPSEETGTTRTVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPKDHGTDPSPFL 300
 DB 241 MLPSPSEETGTTRTVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPKDHGTDPSPFL 300
 QY 301 YSRMLVVKSTWKEKNLVTCRVVHEALPGSRITLSEKSLHYSAGN 342
 DB 301 YSRMLVVKSTWKEKNLVTCRVVHEALPGSRITLSEKSLHYSAGN 342

RESULT 2
 AAB06208
 ID AAB06208 standard; protein; 341 AA.
 AC AAB06208;
 DT 12-SEP-2003 (revised)
 DT 22-NOV-2000 (first entry)
 XX
 DE Immunogenic peptide consisting of opossum CH2, dog CH3 and opossum CH4.
 XX
 KM Dog; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;
 KM asthma; eczema; immunogenic peptide.
 XX
 OS Didelphis virginiana.
 OS Canis sp.
 OS Chimeric.
 OS
 XX WO200025722-A2.
 XX
 PD 11-MAY-2000.
 XX
 PF 21-OCT-1999; 99WO-SR001896.
 XX
 PR 02-NOV-1998; 98US-0106552P.
 PR 22-SEP-1999; 99US-00401636.
 XX
 PA (RESI-) RESISTENTIA PHARM AB.
 XX
 PI Hellman LT;
 XX
 DR WPI; 2000-365342/31.
 XX
 PT Immunogenic polypeptides useful for preventing the harmful effects of
 XX immunoglobulin E in mammals.
 XX
 PS Disclosure; Fig 2; 50pp; English.
 CC The present sequence is an immunogenic peptide consisting of the heavy
 CC chain constant regions 2 and 4 of the opossum Igs and the heavy chain
 CC constant region 3 from the dog. It was shown to cause a stronger
 CC polyclonal anti-self IGF response than peptides consisting of the same

CC regions from one mammal. Immunogenic peptides, particularly those
 CC consisting of different heavy chain constant regions, can be used for
 CC vaccination in humans, against bacterial and viral infections and
 CC allergies, such as asthma, fur, pollen and food allergies and eczema.
 CC (Updated on 12-SEP-2003 to standardise OS field)
 CC
 XX

SQ Sequence 341 AA;
 Query Match 88.6%; Score 1644.5; DB 3; Length 341;
 Best Local Similarity 88.0%; Pred. No. 1.6e-128;
 Matches 301; Conservative 17; Mismatches 23; Indels 1; Gaps 1;

QY 1 EPHHHHHHTLSLPSGSPVITIIPTVTLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60
 DB 1 EPHHHHHHTLSLPSGSPVITIIPTVTLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60
 QY 61 LVVGOBAENLFPTTPKREGGOTFSLQSEVNITOGQMSNTYTCVHNGSIFEDSSR 120
 DB 61 LVVGOBAENLFPTTPKREGGOTFSLQSEVNITOGQMSNTYTCVHNGSIFEDSSR 120
 QY 121 KCADSNPRGVSAVLSRSPSPDLFIRKSPITTCIVDLAPSKGTNLTWSRAGKPVNHS 180
 DB 121 KCADSNPRGVSAVLSRSPSPDLFIRKSPITTCIVDLAPSKGTNLTWSRAGKPVNHS 180
 QY 181 RKEKQRNGTLVTSSTLPVGTDRWINGETVQCRVTHPHLPALMRSTTKLPKRLAPEVY 240
 DB 181 RKEKQRNGTLVTSSTLPVGTDRWINGETVQCRVTHPHLPALMRSTTKLPKRLAPEVY 240
 QY 241 MLPSPSEETGTTRTVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPKDHGTDPSPFL 300
 DB 241 MLPSPSEETGTTRTVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPKDHGTDPSPFL 299
 QY 301 YSRMLVVKSTWKEKNLVTCRVVHEALPGSRITLSEKSLHYSAGN 342
 DB 301 YSRMLVVKSTWKEKNLVTCRVVHEALPGSRITLSEKSLHYSAGN 341

RESULT 3
 AAB06207
 ID AAB06207 standard; protein; 345 AA.
 AC AAB06207;
 DT 12-SEP-2003 (revised)
 DT 22-NOV-2000 (first entry)
 XX
 DE Immunogenic peptide consisting of opossum CH2, pig CH3 and opossum CH4.
 XX
 KM Pig; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;
 KM asthma; eczema; immunogenic peptide.
 XX
 OS Didelphis virginiana.
 OS Sus scrofa.
 OS Chimeric.
 OS
 XX WO200025722-A2.
 XX
 PD 11-MAY-2000.
 XX
 PF 21-OCT-1999; 99WO-SR001896.
 XX
 PR 02-NOV-1998; 98US-0106552P.
 PR 22-SEP-1999; 99US-00401636.
 XX
 PA (RESI-) RESISTENTIA PHARM AB.
 XX
 PI Hellman LT;
 XX
 DR WPI; 2000-365342/31.
 XX
 PT Immunogenic polypeptides useful for preventing the harmful effects of
 XX immunoglobulin E in mammals.
 XX

PS Disclosure; Fig 2; 50bp; English.

XX The present sequence is an immunogenic peptide consisting of the heavy
CC chain constant regions 2 and 4 of the opossum IGE and the heavy chain
CC constant region 3 from the pig. It was shown to cause a stronger
CC polyclonal anti-self IGE response than peptides consisting of the same
CC regions from one mammal. Immunogenic peptides, particularly those
CC consisting of different heavy chain constant regions, can be used for
CC vaccination in humans, against bacterial and viral infections and
CC allergies, such as asthma, fur, pollen and food allergies and eczema.
CC (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 345 AA;

XX Query Match 85.5%; Score 1587.5; DB 3; Length 345;
XX Best Local Similarity 84.7%; Pred. No. 8.8e-124;
XX Matches 298; Conservative 14; Mismatches 23; Indels 17; Gaps 4;

QY 1 EHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60
DB 1 EHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60
QY 61 LVDCGEAENLFPYTRPKREGGQTFSLQSEVNIQGMMSNTYTCVKNHNSIFEDSSR 120
DB 61 LVDCGEAENLFPYTRPKREGGQTFSLQSEVNIQGMMSNTYTCVKNHNSIFEDSSR 120
QY 121 KC-ADSNPRGSAVLSRSPFDLFRKSPITICLVVDLAPSKGTVNLWTSRAS----- 172
DB 121 KC-ADSNPRGSAVLSRSPFDLFRKSPITICLVVDLAPSKGTVNLWTSRAS----- 172
QY 121 RCTASEPRGSAVLSRSPFDLFRKSPITICLVVDLAPSKGTVNLWTSRAS----- 179
DB 121 RCTASEPRGSAVLSRSPFDLFRKSPITICLVVDLAPSKGTVNLWTSRAS----- 179
QY 173 --GKPVNHSRKEEKORNGTLTVSTLPGYTRDMIEGETYQCRVTHPHLPRLMSTTKL 230
DB 173 --GKPVNHSRKEEKORNGTLTVSTLPGYTRDMIEGETYQCRVTHPHLPRLMSTTKL 230
QY 180 PGPEPV-----IKQFNGTFSATSLIPNVSDWIEGETYQCRVTHPHLPRLMSTTKL 233
DB 180 PGPEPV-----IKQFNGTFSATSLIPNVSDWIEGETYQCRVTHPHLPRLMSTTKL 233
QY 231 PKRLAPVEYVLPSPPEETGTRITVCLIRGFYSEISVQWLFNNEEDHTGHTTRPQK 290
DB 231 PKRLAPVEYVLPSPPEETGTRITVCLIRGFYSEISVQWLFNNEEDHTGHTTRPQK 290
QY 234 PKRLAPVEYVLPSPPEETGTRITVCLIRGFYSEISVQWLFNNEEDHTGHTTRPQK 293
DB 234 PKRLAPVEYVLPSPPEETGTRITVCLIRGFYSEISVQWLFNNEEDHTGHTTRPQK 293
QY 291 DSGTDPSPFLYSRMLVKNKSIWEKGLVTCRVVHEALPGSRTLEKSLHYSAGN 342
DB 291 DSGTDPSPFLYSRMLVKNKSIWEKGLVTCRVVHEALPGSRTLEKSLHYSAGN 342
QY 294 DSGTDPSPFLYSRMLVKNKSIWEKGLVTCRVVHEALPGSRTLEKSLHYSAGN 345
DB 294 DSGTDPSPFLYSRMLVKNKSIWEKGLVTCRVVHEALPGSRTLEKSLHYSAGN 345

RESULT 4

XX AAB03644 standard; protein; 341 AA.

XX ID AAB03644;

XX AC AAB03644;

XX DT 22-NOV-2000 (first entry)

XX DE Opossum IGE heavy chain constant regions 2, 3 and 4.

XX OS Opossum; immunoglobulin E; IGE; vaccination; infection; allergy; asthma;

XX KM eczema; immunogenic peptide.

XX OS Didelphis virginiana.

XX OS WO200025722-A2.

XX OS 11-MAY-2000.

XX OS 21-OCT-1999; 99WO-SE001896.

XX OS 02-NOV-1998; 98US-010652P.

XX OS 22-SEP-1999; 99US-00401636.

XX OS (RESI-) RESISTENTIA PHASN AB.

XX OS Hellman LT;

XX OS WPI; 2000-365342/31.

PT Immunogenic polypeptides useful for preventing the harmful effects of
XX immunoglobulin E in mammals.

XX Disclosure; Fig 1; 50bp; English.

XX The present sequence is an immunogenic peptide consisting of the heavy
CC chain constant regions 2, 3 and 4 of the opossum IGE. It was used to
CC construct a number of immunogenic peptides which consisted of regions of
CC IGE from different mammals, which appear to cause a stronger polyclonal
CC anti-self IGE response than peptides consisting of the same regions from
CC one mammal. Immunogenic peptides, particularly those consisting of
CC different heavy chain constant regions, can be used for vaccination in
CC humans, against bacterial and viral infections and allergies, such as
CC asthma, fur, pollen and food allergies and eczema.

XX Sequence 341 AA;

XX Query Match 85.4%; Score 1584.5; DB 3; Length 341;
XX Best Local Similarity 85.1%; Pred. No. 1.5e-123;
XX Matches 291; Conservative 22; Mismatches 28; Indels 1; Gaps 1;

QY 1 EHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60
DB 1 EHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60
QY 61 LVDCGEAENLFPYTRPKREGGQTFSLQSEVNIQGMMSNTYTCVKNHNSIFEDSSR 120
DB 61 LVDCGEAENLFPYTRPKREGGQTFSLQSEVNIQGMMSNTYTCVKNHNSIFEDSSR 120
QY 121 KCADSNPRGSAVLSRSPFDLFRKSPITICLVVDLAPSKGTVNLWTSRAGKPVNHST 180
DB 121 KCADSNPRGSAVLSRSPFDLFRKSPITICLVVDLAPSKGTVNLWTSRAGKPVNHST 180
QY 121 KCDTDPGSAVLSRSPFDLFRKSPITICLVVDLAPSKGTVNLWTSRAGKPVNHST 179
DB 121 KCDTDPGSAVLSRSPFDLFRKSPITICLVVDLAPSKGTVNLWTSRAGKPVNHST 179
QY 181 RKEEKORNGTLTVSTLPGYTRDMIEGETYQCRVTHPHLPRLMSTTKLPGRLAPEYV 240
DB 181 RKEEKORNGTLTVSTLPGYTRDMIEGETYQCRVTHPHLPRLMSTTKLPGRLAPEYV 240
QY 180 LVYKEQYNGFFVTSHLPVNTIDWIEGDTYTCRLSPDMPVLRITISKAPGRLAPEYV 239
DB 180 LVYKEQYNGFFVTSHLPVNTIDWIEGDTYTCRLSPDMPVLRITISKAPGRLAPEYV 239
QY 241 MLPSPPEETGTRITVCLIRGFYSEISVQWLFNNEEDHTGHTTRPQKDGTDSPFL 300
DB 241 MLPSPPEETGTRITVCLIRGFYSEISVQWLFNNEEDHTGHTTRPQKDGTDSPFL 300
QY 240 MLPSPPEETGTRITVCLIRGFYSEISVQWLFNNEEDHTGHTTRPQKDGTDSPFL 299
DB 240 MLPSPPEETGTRITVCLIRGFYSEISVQWLFNNEEDHTGHTTRPQKDGTDSPFL 299
QY 301 YSRMLVKNKSIWEKGLVTCRVVHEALPGSRTLEKSLHYSAGN 342
DB 301 YSRMLVKNKSIWEKGLVTCRVVHEALPGSRTLEKSLHYSAGN 342
QY 300 YSRMLVKNKSIWEKGLVTCRVVHEALPGSRTLEKSLHYSAGN 341
DB 300 YSRMLVKNKSIWEKGLVTCRVVHEALPGSRTLEKSLHYSAGN 341

RESULT 5

XX AAB06206 standard; protein; 341 AA.

XX ID AAB06206;

XX AC AAB06206;

XX DT 12-SEP-2003 (revised)

XX DE 22-NOV-2000 (first entry)

XX OS Immunogenic peptide consisting of opossum CH2, rat CH3 and opossum CH4.

XX KM Rat; Opossum; immunoglobulin E; IGE; vaccination; infection; allergy;

XX OS asthma; eczema; immunogenic peptide.

XX OS Didelphis virginiana.

XX OS Ratcua sp.

XX OS Chimeric.

XX OS WO200025722-A2.

XX OS 11-MAY-2000.

XX OS 21-OCT-1999; 99WO-SE001896.

XX OS 02-NOV-1998; 98US-010652P.

XX OS 22-SEP-1999; 99US-00401636.

(RESI-) RESISTENTIA PHARM AB.
 Hellman LT;
 WPI, 2000-365342/31.
 Immungenic polypeptides useful for preventing the harmful effects of
 immunoglobulin E in mammals.
 Disclosure, Fig 2, 50pp; English.
 The present sequence is an immunogenic peptide consisting of the heavy
 chain constant regions 2 and 4 of the opossum IGE and the heavy chain
 constant region 3 from the rat. It was shown to cause a stronger
 polyclonal anti-self IGE response than peptides consisting of the same
 regions from one mammal. Immunogenic peptides, particularly those
 consisting of different heavy chain constant regions, can be used for
 vaccination in humans, against bacterial and viral infections and
 allergies, such as asthma, fur, pollen and food allergies and eczema.
 (Updated on 12-SEP-2003 to standardise OS field)
 Sequence 341 AA;
 Query Match 84.5%; Score 1568.5; DB 3; Length 341;
 Best Local Similarity 83.3%; Pred. No. 3.3e-122;
 Matches 285; Conservative 20; Mismatches 36; Indels 1; Gaps 1;
 1 EFHHHHHTLSPESGPTIIPPTVKLFHSSCDPRGDAHSTIOLLCVSGSPAKVHTW 60
 1 EFHHHHHTLSPESGPTIIPPTVKLFHSSCDPRGDAHSTIOLLCVSGSPAKVHTW 60
 61 LVDSGEANLPPYTRPRREGGQFSLQSEVNTIQGOWMSNTYTCVHNGSIFEDSR 120
 61 LVDSGEANLPPYTRPRREGGQFSLQSEVNTIQGOWMSNTYTCVHNGSIFEDSR 120
 121 KCADSNPGRVSAVSRPSFDLFRKSPPTTCLVVDIAPSKGTVNLTWSPASGKPVNHS 180
 121 RCDSDPRGVTITLPPSPDLVYENGPKITCLVLDL-ESEENITVWVERKKSIGSAS 179
 181 RREKQRNGTLVNSTLVGTRDWIEGTYOCRTVHPHLRALMRSTTKLPGRLAPEV 240
 181 RREKQRNGTLVNSTLVGTRDWIEGTYOCRTVHPHLRALMRSTTKLPGRLAPEV 240
 180 CRSTGHNAITSISILPVDKMDIEGTYOCRTVHPHLRALMRSTTKLPGRLAPEV 239
 241 MLPSPESTGTRTYTCLIRGFYSEISVQWLFNNEEDTGHHTTRPQDGTDSFPL 300
 240 MLPSPESTGTRTYTCLIRGFYSEISVQWLFNNEEDTGHHTTRPQDGTDSFPL 299
 301 YSRMLVNSIWEKGNLVTCRVVHEALPGSRTEKSLHYSAGN 342
 300 YSRMLVNSIWEKGNLVTCRVVHEALPGSRTEKSLHYSAGN 341
 RESULT 6
 ABP96587
 ID ABP96587 standard; protein; 446 AA.
 AC ABP96587;
 XX
 DT 28-MAY-2003 (first entry)
 DE Opossum IGE heavy chain amino acid sequence SEQ ID NO:32.
 XX
 KW Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;
 KW immune response; major histocompatibility complex; MHC; immunogenic;
 KW anti-allergic; anti-inflammatory; immunosuppressive; vasoactive; cytostatic;
 KW dermatological; anti-inflammatory; IGF-mediated condition; food allergy;
 KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
 KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
 KW urticaria hives.
 OS Monodelphis domestica.
 XX
 PN WO2003015716-A2.

XX 27-FEB-2003.
 PD 08-AUG-2002; 2002WO-US026986.
 XX 13-AUG-2001; 2001US-0312120P.
 PR (IGET-) IGE THERAPEUTICS INC.
 PA Chen SA, Yang Y, Barankiewicz T, Chen Z,
 PI WPI, 2003-268242/26.
 PS
 XX
 CC The present invention describes a method (M1) for identifying peptides
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
 CC E (IGE), comprising providing a test peptide (T) suspected of being able
 CC to bind to major histocompatibility complex (MHC) class I molecule, and
 CC evaluating (T) for ability to elicit in a mammal a CTL response to
 CC naturally processed and presented IGE peptides, where a peptide that
 CC induces such a response is identified. Also described are compositions:
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and
 CC (C3) comprising antigen-presenting cells that recognise at least one (I).
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to
 CC elicit in a mammal a CTL response to naturally processed and presented
 CC IGE peptides, C1-3 have anti-allergic, antiasthmatic, immunosuppressive,
 CC vasoactive, dermatological, anti-inflammatory and cytostatic activities,
 CC and can be used as inducers of a CTL response against IGE, and in
 CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a
 CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as
 CC IGE-mediated atopic hypersensitivity condition, IGF-mediated non-atopic
 CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are
 CC useful for treating atopic hypersensitivity conditions (such as allergic
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
 CC hives). The present sequence represents an IGE heavy chain amino acid
 CC sequence, which is given in an example from the present invention
 CC
 XX
 XX
 Sequence 446 AA;
 Query Match 82.1%; Score 1523.5; DB 6; Length 446;
 Best Local Similarity 84.7%; Pred. No. 2.6e-118;
 Matches 283; Conservative 21; Mismatches 29; Indels 1; Gaps 1;
 9 TSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIOLLCVSGSPAKVHTWLDGQAE 68
 114 TSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIOLLCVSGSPAKVHTWLDGQAE 173
 69 NLFPYTRPRREGGQFSLQSEVNTIQGOWMSNTYTCVHNGSIFEDSRKCADSNPR 128
 174 NLFPYTRPRREGGQFSLQSEVNTIQGOWMSNTYTCVHNGSIFEDSRKCADSNPR 233
 129 GVSAYLSRPSFDLFRKSPPTTCLVVDIAPSKGTVNLTWSPASGKPVNHSRBEKQRN 186
 234 GVSAYLSRPSFDLFRKSPPTTCLVVDIAPSKGTVNLTWSPASGKPVNHSRBEKQRN 292
 189 GTITVNSTLVGTRDWIEGTYOCRTVHPHLRALMRSTTKLPGRLAPEVYMLPPSPDE 248
 293 GTITVNSTLVGTRDWIEGTYOCRTVHPHLRALMRSTTKLPGRLAPEVYMLPPSPDE 352
 249 TGTTRTYTCLIRGFYSEISVQWLFNNEEDTGHHTTRPQDGTDSFPLYSRMLVNS 308
 353 TGTTRTYTCLIRGFYSEISVQWLFNNEEDTGHHTTRPQDGTDSFPLYSRMLVNS 412
 309 SIWEKGNLVTCRVVHEALPGSRTEKSLHYSAGN 342

Db 413 STMEKGNLVTGCRVHEALPGSRITLKSILHYSAGN 446

RESULT 7
AAB06202

ID AAB06202 standard; protein; 341 AA.

XX AAB06202;

DT 12-SEP-2003 (revised)

DT 22-NOV-2000 (first entry)

XX Immunogenic peptide consisting of opossum CH2, mouse CH3 and opossum CH4.

XX Mouse; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;
XX asthma; eczema; immunogenic peptide.

XX Didelphis virginiana.

XX Mus sp.

XX Chimeric.

FH Key Location/Qualifiers

FT Misc-difference 1..341
/label= OTHER

/note= "Xaa=unknown"

XX MO200025722-A2.

XX 11-MAY-2000.

XX 21-OCT-1999; 99WO-SE001896.

XX 02-NOV-1998; 98US-0106652P.

XX 22-SEP-1999; 99US-00401636.

XX (RESI-) RESISTENTIA PHARM AB.

XX Hellman LT;

XX MPI; 2000-365342/31.

XX Immunogenic polypeptides useful for preventing the harmful effects of
XX immunoglobulin E in mammals.

XX Disclosure; Fig 2; 50pp; English.

XX The present sequence is an immunogenic peptide consisting of the heavy
 XX chain constant regions 2 and 4 of the opossum IgE and the heavy chain
 XX constant region 3 from the mouse. It was shown to cause a stronger
 XX polyclonal anti-self IgE response than peptides consisting of the same
 XX regions from one mammal. Immunogenic peptides, particularly those
 XX consisting of different heavy chain constant regions, can be used for
 XX vaccination in humans, against bacterial and viral infections and
 XX allergies, such as asthma, fur, pollen and food allergies and eczema.
 XX (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 341 AA;

Query Match 75.0%; Score 1392.5; DB 3; Length 341;

Best Local Similarity 76.7%; Pred. No. 1.5e-107;

Matches 263; Conservative 22; Mismatches 53; Indels 5; Gaps 3;

QY 1 EFHHHHHTLSPESGPTTTPPYKLFHSCDRGDASHITQLCLVSGSPAKVAVTW 60

Db 1 EFHHHHHTLSPESGPTTTPPYKLFHSCDRGDASHITQLCLVSGSPAKVAVTW 60

QY 61 LVDGGEAENLFPYTRPRGEGGTFSLQSEVNITQGMMSNTYTCVKNNGSIFEDSSR 120

Db 61 LVDGGEAENLFPYTRPRGEGGTFSLQSEVNITQGMMSNTYTCVKNNGSIFEDSSR 120

QY 121 KCADSNPFGCAVYLSRSPFDFLTKRSPTTCLVVDLAPSKGVNLTWASAGKPVVHST 180

Db 121 RCPHPRGVITVYLPSPDLVYOHGAPKLTCLVLDSEK-HINVTWNG--KPTXXA 177

QY 181 RK--BEKORNGTLTSTLPVGRDMEIGETVQCRVTHPHLPALMRSTTKLPGKLAPE 238

Db 178 XQMYTHHHHATXISILPVAKQWIEGYXQIXDHPKXKXVSTTRLPGRKLAX 237

QY 239 VYMLPPSPERTGTTTTCILIRGYPSEISVOMLFNNEEDHTGHTTTPQKHGTDPSP 298

Db 238 VYMLPPSPERTGTTTTCILIRGYPSEISVOMLFNNEEDHTGHTTTPQKHGTDPSP 297

QY 299 FLYSRMLVNSKSTMEKGNLVTGCRVHEALPGSRITLKSILHYSAG 341

Db 298 FLYSRMLVNSKSTMEKGNLVTGCRVHEALPGSRITLKSILHYSAG 340

RESULT 8
AAB06201

ID AAB06201 standard; protein; 342 AA.

XX AAB06201;

DT 12-SEP-2003 (revised)

DT 22-NOV-2000 (first entry)

XX Immunogenic peptide consisting of opossum CH2, CH4 and rat/opossum CH3.
XX Rat; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;
XX asthma; eczema; immunogenic peptide.

XX Didelphis virginiana.

XX Rattus sp.

XX Chimeric.

FH Key Location/Qualifiers

FT Misc-difference 1..342
/label= OTHER

/note= "Xaa=unknown"

XX MO200025722-A2.

XX 11-MAY-2000.

XX 21-OCT-1999; 99WO-SE001896.

XX 02-NOV-1998; 98US-0106652P.

XX 22-SEP-1999; 99US-00401636.

XX (RESI-) RESISTENTIA PHARM AB.

XX Hellman LT;

XX MPI; 2000-365342/31.

XX Immunogenic polypeptides useful for preventing the harmful effects of
XX immunoglobulin E in mammals.

XX Disclosure; Fig 2; 50pp; English.

XX The present sequence is an immunogenic peptide consisting of the heavy
 XX chain constant regions 2 and 4 of the opossum IgE and the heavy chain
 XX constant region 3 created from a combination of the one from the rat and
 XX the one from the opossum. It was shown to cause a stronger polyclonal
 XX anti-self IgE response than peptides consisting of the same regions from
 XX one mammal. Immunogenic peptides, particularly those consisting of
 XX different heavy chain constant regions, can be used for vaccination in
 XX humans, against bacterial and viral infections and allergies, such as
 XX asthma, fur, pollen and food allergies and eczema. (Updated on 12-SEP-
 XX 2003 to standardise OS field)

XX Sequence 342 AA;

Query Match 74.1%; Score 1375; DB 3; Length 342;

Best Local Similarity 76.6%; Pred. No. 4.4e-106;
Matches 262; Conservative 23; Mismatches 55; Indels 2; Gaps 2;

CC 1 EFNHHHTLSIPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTM 60
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and
 CC (C3) comprising antigen-presenting cells that recognize at least one (I).
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to
 CC elicit in a mammal a CTL response to naturally processed and presented
 CC Igs peptides, C1-3 have anti-allergic, antiaesthetic, immunosuppressive,
 CC vasoatropic, dermatological, anti-inflammatory and cytostatic activities,
 CC and can be used as inducers of a CTL response against Igs, and in
 CC vaccines. C1-3 are useful for modulating an Igs-mediated condition in a
 CC mammal. C1-3 are useful for modulating an Igs-mediated condition such as
 CC Igs-mediated atopic hypersensitivity condition, Igs-mediated non-atopic
 CC hypersensitivity condition, Igs myeloma in a mammal. Preferably, C1-3 are
 CC useful for treating atopic hypersensitivity conditions (such as allergic
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
 CC hives). The present sequence represents an Igs heavy chain amino acid
 CC sequence, which is given in an example from the present invention

CC Sequence 427 AA;
 SQ

Query Match 69.3%; Score 1285.5; DB 6; Length 427;
 Best Local Similarity 69.6%; Pred. No. 176-98;
 Matches 234; Conservative 47; Mismatches 52; Indels 3; Gaps 2;

CC 1 EFNHHHTLSIPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTM 60
 CC 1 EFNHHHTLSIPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTM 60
 CC 61 LVDGGEAENLPYTRPRREGGQFSLQSEVNITQGMWSSNTYTCVKHNGSIFEDSR 120
 CC 61 LVDGGEAENLPYTRPRREGGQFSLQSEVNITQGMWSSNTYTCVKHNGSIFEDSR 120
 CC 121 KADSNPRGVSAYLSRPSFPDLFRKSPITTCVLVDIAPSKGTYNLTWSRASKPVNHS 180
 CC 121 KADSNPRGVSAYLSRPSFPDLFRKSPITTCVLVDIAPSKGTYNLTWSRASKPVNHS 180
 CC 121 RQSDDEPRGVITVLLPSPDLRYHGTGPKLCLVDL-EESEHIXVTVVXERPKXIGXAR 179
 CC 181 RREKQR-NGTLTSTPVGTRDWIEGETYQCVTHPHPALMRSTTLPGKRLAPRY 239
 CC 181 RREKQR-NGTLTSTPVGTRDWIEGETYQCVTHPHPALMRSTTLPGKRLAPRY 239
 CC 180 SLVVEKXHGFTXSHLPVETDMDIKXTYXXLESFDMVILLPTSLPKRLAPRY 239
 CC 240 YMLPSPSPERTGTRVTCCLINGFPSEISVQWLFNNEBDTHHTTRPOKHGTDPSFP 299
 CC 240 YMLPSPSPERTGTRVTCCLINGFPSEISVQWLFNNEBDTHHTTRPOKHGTDPSFP 299
 CC 240 YMLPSPSPERTGTRVTCCLINGFPSEISVQWLFNNEBDTHHTTRPOKHGTDPSFP 299
 CC 300 LYSRMLVNSKIWEKGNLVTGCVVHEALPGSRTLEKSLHYAG 341
 CC 300 LYSRMLVNSKIWEKGNLVTGCVVHEALPGSRTLEKSLHYAG 341
 CC 300 LYSRMLVNSKIWEKGNLVTGCVVHEALPGSRTLEKSLHYAG 341

RESULT 9
 ABP96591
 ID ABP96591 standard; protein; 427 AA.
 AC ABP96591;
 DT 28-MAY-2003 (first entry)
 XX

DE Brushcail possum Igs heavy chain amino acid sequence SEQ ID NO:36.
 KW Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;
 KW immune response; major histocompatibility complex; MHC; immunogenic;
 KW anti-allergic; antiaesthetic; immunosuppressive; vasoatropic; cytostatic;
 KW dermatological; anti-inflammatory; Igs-mediated condition; food allergy;
 KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
 KW urticaria hives.
 KW

OS Trichosurus vulpecula.
 XX
 XX WO2003015716-A2.
 XX
 XX 27-FEB-2003.
 XX
 XX 08-AUG-2002; 2002MO-US026986.
 XX
 XX 13-AUG-2001; 2001US-0312120P.
 XX
 XX (IGET-) IGE THERAPEUTICS INC.
 XX
 XX Chen SA, Yang Y, Barankiewicz T, Chen Z;
 XX
 XX MPI; 2003-268242/26.
 XX

PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
 PT against Igs, by identifying peptide eliciting CTL response to Igs
 PT peptides naturally presented by major histocompatibility complex class I
 PT protein.
 XX
 XX Example 7; Page 172-174; 187pp; English.
 XX
 XX The present invention describes a method (M1) for identifying peptides
 XX that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
 XX E (Igs), comprising providing a test peptide (I) suspected of being able
 XX to bind to major histocompatibility complex (MHC) class I molecule, and
 XX evaluating (I) for ability to elicit in a mammal a CTL response to
 XX naturally processed and presented Igs peptides, where a peptide that

CC induces such a response is identified. Also described are compositions:
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and
 CC (C3) comprising antigen-presenting cells that recognize at least one (I).
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to
 CC elicit in a mammal a CTL response to naturally processed and presented
 CC Igs peptides, C1-3 have anti-allergic, antiaesthetic, immunosuppressive,
 CC vasoatropic, dermatological, anti-inflammatory and cytostatic activities,
 CC and can be used as inducers of a CTL response against Igs, and in
 CC vaccines. C1-3 are useful for modulating an Igs-mediated condition in a
 CC mammal. C1-3 are useful for modulating an Igs-mediated condition such as
 CC Igs-mediated atopic hypersensitivity condition, Igs-mediated non-atopic
 CC hypersensitivity condition, Igs myeloma in a mammal. Preferably, C1-3 are
 CC useful for treating atopic hypersensitivity conditions (such as allergic
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
 CC hives). The present sequence represents an Igs heavy chain amino acid
 CC sequence, which is given in an example from the present invention

CC Sequence 427 AA;
 SQ

Query Match 69.3%; Score 1285.5; DB 6; Length 427;
 Best Local Similarity 69.6%; Pred. No. 176-98;
 Matches 234; Conservative 47; Mismatches 52; Indels 3; Gaps 2;

CC 7 HHTLSIPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTM 66
 CC 7 HHTLSIPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTM 66
 CC 95 HVSTGPTKNGPV--IPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTM 152
 CC 95 HVSTGPTKNGPV--IPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTM 152
 CC 67 AENLPYTRPRREGGQFSLQSEVNITQGMWSSNTYTCVKHNGSIFEDSRKCADSN 126
 CC 67 AENLPYTRPRREGGQFSLQSEVNITQGMWSSNTYTCVKHNGSIFEDSRKCADSN 126
 CC 153 AENLPYTRPRREGGQFSLQSEVNITQGMWSSNTYTCVKHNGSIFEDSRKCADSN 212
 CC 153 AENLPYTRPRREGGQFSLQSEVNITQGMWSSNTYTCVKHNGSIFEDSRKCADSN 212
 CC 127 PRGVSAYLSRPSFPDLFRKSPITTCVLVDIAPSKGTYNLTWSRASKPVNHS 186
 CC 127 PRGVSAYLSRPSFPDLFRKSPITTCVLVDIAPSKGTYNLTWSRASKPVNHS 186
 CC 213 PRGVSAYLSRPSFPDLFRKSPITTCVLVDIAPSKGTYNLTWSRASKPVNHS 271
 CC 213 PRGVSAYLSRPSFPDLFRKSPITTCVLVDIAPSKGTYNLTWSRASKPVNHS 271
 CC 187 RGLTAVTSTLPVGTDMWIEGETYQCVTHPHPALMRSTTLPGKRLAPRY 246
 CC 187 RGLTAVTSTLPVGTDMWIEGETYQCVTHPHPALMRSTTLPGKRLAPRY 246
 CC 272 YNGVITVITSLPQTDWIEGETYQCVTHPHPALMRSTTLPGKRLAPRY 331
 CC 272 YNGVITVITSLPQTDWIEGETYQCVTHPHPALMRSTTLPGKRLAPRY 331
 CC 247 EFGTTRVTCCLINGFPSEISVQWLFNNEBDTHHTTRPOKHGTDPSFP 306
 CC 247 EFGTTRVTCCLINGFPSEISVQWLFNNEBDTHHTTRPOKHGTDPSFP 306
 CC 332 EERKNTVITVITSLPQTDWIEGETYQCVTHPHPALMRSTTLPGKRLAPRY 391
 CC 332 EERKNTVITVITSLPQTDWIEGETYQCVTHPHPALMRSTTLPGKRLAPRY 391
 CC 307 NKSIMEKGNLVTGCVVHEALPGSRTLEKSLHYAG 342
 CC 307 NKSIMEKGNLVTGCVVHEALPGSRTLEKSLHYAG 342
 CC 392 NRSWMOGHFTFCRVVHEALPGSRTLEKSLHYAG 427
 CC 392 NRSWMOGHFTFCRVVHEALPGSRTLEKSLHYAG 427

RESULT 10
 AA019668
 ID AA019668 standard; protein; 569 AA.
 AC AA019668;
 DT 28-MAR-2003 (first entry)
 XX

DE G22 fusion protein for use in treating immune diseases.
 KW Human; IGE; immunoglobulin E; immunotherapy; immune disease;
 KW Fc receptor; autoimmune disease; constant region; heavy chain;
 KW antiaesthetic; anti-allergic; anti-inflammatory; dermatological; G22;
 KW antiaesthetic; antirheumatic; antidiabetic; neuroprotective;
 KW fusion protein.
 XX
 XX Synthetic.
 XX Undifferentiated.
 XX WO200288317-A2.
 XX
 XX 07-NOV-2002.
 XX

PF		01-MAY--2002; 2002WO-USO13527.
XX		
PR	01-MAY-2001; 2001US-00847208-	
PR	24-OCT-2001; 2001US-00000439.	
XX		
PA	(REGC) UNIV CALIFORNIA.	
XX		
PI	Saxon A, Zhang K, Zhu D;	
DR	WPI, 2003-103456/09.	
XX		
PT	New fusion molecules comprising polypeptide sequences that bind to IgG	
PT	inhibitory receptor and native IgE receptor, useful for treating IgE-	
PT	mediated hypersensitivity reactions, e.g. asthma or allergies, or	
PT	autoimmune diseases.	
XX		
PS	Claim 35; Fig 7; 116pp; English.	
XX		
CC	The present invention relates to a fusion molecule comprising a first	
CC	polypeptide sequence capable of specific binding to a native IgE	
CC	inhibitory receptor consisting of an immune receptor tyrosine-based	
CC	inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,	
CC	functionally connected to a second polypeptide sequence capable of	
CC	specific binding directly or indirectly to a native IgE receptor	
CC	(Fc ϵ s1a). Also provided are nucleotide sequences encoding such a	
CC	fusion protein. The fusion molecules and compositions are useful for	
CC	treating an IgE-mediated biological response, preferably an IgE-mediated	
CC	hypersensitivity reaction, such as asthma, allergic rhinitis, atopic	
CC	dermatitis, severe food allergies, chronic urticaria, angioedema or	
CC	anaphylactic shock, or autoimmune diseases such as rheumatoid arthritis,	
CC	type-1 diabetes mellitus, or multiple sclerosis, and for preventing of,	
CC	or symptoms resulting from, a type I hypersensitivity reaction in a	
CC	subject receiving immunotherapy. The present sequence is a gammahinge-	
CC	CHgamma2-CHgamma3-(GlySer)3-Chep1lon2-Chep1lon3 fusion	
CC	protein (designated GE2) of the invention	
CC		
XX		
SQ	Sequence 569 AA;	
	Query Match	56.3%; Score 1045.5; DB 6; Length 569;
	Best Local Similarity	58.0%; Pred. No. 2.3e-78;
	Matches 206; Conservative 45; Mismatches 83; Indels 21; Gaps 5;	
OY	HHHHHNTSLP-----ESGPVTHIPEPTVLFFHSQCDPRDASTLOLCLV 48	
DB	219 NHYQORSLSLSPGKRYEGGGSGGGSGGGSTPTPVTKILQSSCGGGHPFTTOLLCLV 278	
OY	49 SGSPDAKVHWLVLDGQEAENLFPTTRPKRGGQTFSLOSSEVNITQGOMSSNITYYCHV 108	
DB	279 SGYPGTGINITWLEDGGVMD--VDLSLTASTTOEGELASTOSHLISOKHWNIDRTYTQCV 336	
OY	109 KHNSIFEDSRKCADSNPRGVSAVLSAPSPDDLIRKSPPTTCVLVDLABSKGVNLTM 168	
DB	337 TYOGHTFEDSDIRKKCADSNPRGVSAVLSPPSPDLLIRKSPTITCLVVDLABSKGVNLTM 396	
OY	169 SPASGKPVNSTRKEEKORNGTLVTYSTLPVGSTRDMIGETTYQQCKVTPHPLPALMRSTT 228	
DB	397 SRASGKPVNSTRKEEKORNGTLVTYSTLPVGSTRDMIGETTYQQCKVTPHPLPALMRSTT 456	
OY	229 KLPGRIALPEYYMLPSPSEETGT--TRTVTCLIRGFYSSEISVQWLFINNEHDHGHHTTT 286	
DB	457 KTSGPRALPEYYAFATPEPDGSRKRLTACLICQFMEDDISVQWLAHEVCJDPDARSHST 515	
OY	287 RPQKHGDGPSFFLYSRMLYNKSIWEKNLVTCRVVHAALPDSRTLEKSLHYASG 341	
DB	516 QPKTKGS--GFVFVSRLLEVTRAWEQKDEFCRAVHAASPSQTVQRAVSVNPQ 568	
RESULT 11		
ID	ABP96584	
XX	ABP96584 standard; protein; 577 AA.	
XX	ABP96584;	

28-MAY-2003 (first entry)
Duckbilled platypus Ige heavy chain amino acid sequence SEQ ID NO:29.
Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;
immune response; major histocompatibility complex; MHC; immunogenic;
antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;
dermatological; antiinflammatory; IgE-mediated condition; food allergy;
atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
urticaria hives.

Omithorhynchus anatinus.
WO2003015716-A2.
27-FEB-2003.
08-AUG-2002; 2002MO-US026986.
13-AUG-2001; 2001US-0312120P.
(IGET-) IGE THERAPEUTICS INC.
Chen SA, Yang Y, Barankiewicz T, Chen Z;
WPI, 2003-268242/26.

The present invention describes a method (M1) for identifying peptides that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin E (IgE), comprising providing a test peptide (T) suspected of being able to bind to major histocompatibility complex (MHC) class I molecule, and evaluating (T) for ability to elicit in a mammal a CTL response to naturally processed and presented Ige peptides, where a peptide that induces such a response is identified. Also described are compositions: (C1) comprising at least one immunogenic peptide (I) identified by (M1); (C2) comprising at least one isolated polynucleotide encoding (I); and (C3) comprising antigen-presenting cells that recognise at least one (I). Where C1-3 are able to bind to at least one MHC class I molecule and to elicit in a mammal a CTL response to naturally processed and presented Ige peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive, vasotropic, dermatological, antiinflammatory and cytostatic activities, and can be used as inducers of a CTL response against Ige, and in vaccines. C1-3 can be used for modulating an Ige-mediated condition in a mammal. C1-3 are useful for modulating an Ige-mediated condition such as Ige-mediated atopic hypersensitivity condition. Ige-mediated non-atopic hypersensitivity condition, Ige myeloma in a mammal. Preferably, C1-3 are useful for treating atopic hypersensitivity conditions (such as allergic rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-atopic hypersensitivity conditions (such as anaphylaxis, and urticaria hives). The present sequence represents an Ige heavy chain amino acid sequence, which is given in an example from the present invention

Sequence 577 AA,
Query Match 56.2%; Score 1044; DB 6; Length 577;
Best Local Similarity 57.4%; Pred. No. 3.2e-78;
Matches 187; Conservative % 63; Mismatches 70; Indels 6; Gaps 4;

1 IIPVYKLFHSSCDPRGASHSTLTCLCVSGSPAKHYVTMLVDQEAENLFPYTTPRRE 80
DB 254 IIPVYKLHSSCDPRGSQSAILLCILITGTSPIGVIOVMVLVDQCKENLPFYAPPRRE 313
GY GGQTFSLSQSEVNITQGQMSNTTYCHVKY--NCSIFEDSSRKCADSNFRVSAYLSRPS 138
DB 314 GNRFSSHSEVNITQDOWLISGRTTCOVTHLADKKTVDSARKKCADSPRRITVEFLTPS 373

QY 139 PFDLFRKSPITTCVVDLAPSKGTUNLTWRSAGKPVNSTRKEKORNGTLTVSTLP 198
 DB 374 PFDLYISKPTKLTCLIIDVSTEG-MEYTWRSRSTPLASPEEQFGNTMSFISTV 432
 QY 199 VGRDRIEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVYMLPSPPEET--GTRIVY 256
 DB 433 VNIQDNESGTYTCVAVHDLPSPIKIVTLPKRLAPEVYAFPPQAVSHGDSLSLT 492
 QY 257 CLIRGYPSISVQVLFNNEEDHTGHTTTPQCDHGDSPFLLYSKMLVNSIWEKGNL 316
 DB 493 CLIRGYPSISVQVLFNNEEDHTGHTTTPQCDHGDSPFLLYSKMLVNSIWEKGNL 552
 QY 317 VTCRVVHEALPGSRTELEKSLHYSAGN 342
 DB 553 YTCQVVEHALP-SRMTERRKFGHTSGN 577

RESULT 12
 ID AA019667 standard; protein; 320 AA.
 AC AA019667;
 XX
 DT 28-MAR-2003 (first entry)
 DE Human IgE heavy chain constant region CH2-CH3-CH4 portion.
 XX
 KW Human IgE; immunoglobulin E; immunotherapy; immune disease;
 KW Fc epsilon receptor; autoimmune disease; constant region; heavy chain;
 KW antisthmatic; antiallergic; antiinflammatory; dermatological;
 KW anaphylactic; antineumatic; antidiabetic; neuroprotective;
 KW CH2-CH3-CH4 region.
 XX
 OS Homo sapiens.
 XX
 PN WO200288317-A2.
 XX
 PD 07-NOV-2002.
 XX
 PF 01-MAY-2002; 2002WO-US013527.
 XX
 PR 01-MAY-2001; 2001US-00847208.
 XX
 PR 24-OCT-2001; 2001US-00000439.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Saxon A, Zhang K, Zhu D;
 XX
 DR WPI; 2003-103456/09.
 XX
 PT New fusion molecules comprising polypeptide sequences that bind to IgE
 PT inhibitory receptor and native IgE receptor, useful for treating IgE-
 PT mediated hypersensitivity reactions, e.g. asthma or allergies, or
 PT autoimmune diseases.
 XX
 PS Claim 21; Fig 6; 116pp; English.
 XX
 CC The present invention relates to a fusion molecule comprising a first
 CC polypeptide sequence capable of specific binding to a native IgE
 CC inhibitory receptor consisting of an immune receptor tyrosine-based
 CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
 CC functionally connected to a second polypeptide sequence capable of
 CC specific binding directly or indirectly to a native IgE receptor
 CC (Fc epsilon receptor). Also provided are nucleotide sequences encoding such a
 CC fusion protein. The fusion molecules and compositions are useful for
 CC treating an IgE-mediated biological response, preferably an IgE-mediated
 CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic
 CC dermatitis, severe food allergies, chronic urticaria, angioedema or
 CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
 CC type-1 diabetes mellitus, or multiple sclerosis, and for preventing of,
 CC or symptoms resulting from, a type I hypersensitivity reaction in a
 CC subject receiving immunotherapy. The present sequence is the human IgE

CC heavy chain constant region CH2-CH3-CH4 portion
 XX
 SQ Sequence 320 AA;
 Query Match 56.0%; Score 1038.5; DB 6; Length 320;
 Best Local Similarity 62.4%; Pred. No. 4.3e-78;
 Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;

QY 22 PPTKLFHSSCDPRGDAHSTTQLCLVSGSPAKVHTVLVDQDAENLPYTRPKRSG 81
 DB 3 PPYKLIQSSCDGGHPPITQLCLVSGYTPGTINITLWEDGVWD--VDLSTASTQ 60
 QY 82 GQFSLQSEVNIQGGWMSNTYTCVKNNGSIFEDSSKCKADSNPRGVSAVLSPPFD 141
 DB 61 GELASTQSELTQKMLSDRTTCQVYQGHFEDSTKCKADSNPRGVSAVLSPPFD 120
 QY 142 LFIKSPITTCVVDLAPSKGTUNLTWRSAGKPVNSTRKEKORNGTLTVSTLP 201
 DB 121 LFIKSPITTCVVDLAPSKGTUNLTWRSAGKPVNSTRKEKORNGTLTVSTLP 180
 QY 202 RDMIEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVYMLPSPPEET--TRIVTCL 259
 DB 181 RDMIEGETYQCRVTHPHLPALMRSTTKSGRAAPEVYAF-ATPEWPSRDKRLACLI 239
 QY 260 RGFYPSISVQVLFNNEEDHTGHTTTPQCDHGDSPFLLYSKMLVNSIWEKGNL 319
 DB 240 QNFPEEDISVQVLFNNEEDHTGHTTTPQCDHGDSPFLLYSKMLVNSIWEKGNL 297
 QY 320 RVVHEALPGSRTELEKSLHYSAGN 341
 DB 298 RAVHEALPGSQTVQRAVSVNRG 319

RESULT 13
 ID AA080286 standard; protein; 323 AA.
 AC AA080286;
 XX
 DT 30-JUL-2002 (first entry)
 DE Human IgE C2-C3-C4 domains for E.Coli expression.
 XX
 KW IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
 KW antisthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;
 KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
 KW heavy chain C domain.
 XX
 OS Homo sapiens.
 XX
 PN Synthetic.
 XX
 PN WO200220038-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 06-SEP-2001; 2001WO-DK000579.
 XX
 PR 06-SEP-2000; 2000DK-00003326.
 XX
 PR 15-SEP-2000; 2000US-0232831P.
 XX
 PA (PHAR-) PHARMEXA AS.
 XX
 PI Klyener S, Von Hoegen P, Voldborg B, Gautam A;
 XX
 DR WPI; 2002-383033/41.
 XX
 DR N-Psdb; ABK51134.
 XX
 PT Inducing immune response against autologous immunoglobulin E in an
 PT animal, by effecting simultaneous presentation of cytotoxic T lymphocyte
 PT epitope an/or B-cell epitope derived from the immunoglobulin.
 XX
 PS Disclosure; Page 112-113; 151pp; English.
 XX

CC This invention relates to a novel method for inducing an immune response
 CC against autologous immunoglobulin E (IgE) in an animal. The method
 CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte
 CC (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell
 CC epitope (TH epitope) which is foreign to the animal, by antigen
 CC presenting cells (APCs) of the animal's immune system. The epitopes of
 CC the invention may be used as a vaccine against allergic diseases. The
 CC method of the invention is useful for inducing an immune response against
 CC autologous IgE in an animal, which is useful for downregulating
 CC autologous IgE in the animal. This method is useful in the prevention and
 CC treatment of allergic diseases such as anaphylaxis, allergic rhinitis,
 CC asthma and atopic dermatitis. The present sequence represents the human
 CC IgE heavy chain C2-C3-C4 domains optimised for expression in an E. Coli
 CC system, this sequence was used to create the epitopes of the invention
 XX
 SQ Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;
 Best Local Similarity 62.4%; Pred. No. 4,3e-78;
 Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;

QY 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTWLVGQEAENLFYTRPRKRG 81
 DB 6 PPTVKLIQSSCDGGHFPPTIQLCLVSGYTPGTINITWLBQVMD--VDLSTASTQ 63
 QY 82 GQTFSLQSEVNTQCGMSSNTYTCVYKNGSIFEDSRKCADSNPRGVSAVLSRPPFD 141
 DB 64 GELASTQSELTLSQKHWLSDRTYTQVYQGHTEFDSYRKCADSNPRGVSAVLSRPPFD 123
 QY 142 LFIKSPITTCVLDVLAASKGTVNLTWGRASGKPVNHSRKEKORNGTLVTSILPVG 201
 DB 124 LFIKSPITTCVLDVLAASKGTVNLTWGRASGKPVNHSRKEKORNGTLVTSILPVG 183
 QY 202 RDMWIGETVQCRVTHPHLPALMRSTYKLPGRALAPVYMLPSPDETGT--TRTVGLI 259
 DB 184 RDMWIGETVQCRVTHPHLPALMRSTYKLPGRALAPVYMLPSPDETGT--TRTVGLI 242
 QY 260 RGFYSEISVQWLFNNEBDHTGHTTTRPOKHGDPSPFLYSRLVKSIMWKNLVTVC 319
 DB 243 QNFMEEDISVQWLNHEVQLPDARHSTTOPRKTKS--GFVFSRLVTRAEWQKDEFTIC 300
 QY 320 RVVHEALPGSRTLEKSLHYSAG 341
 DB 301 RAVHEAASPSQTVQRAVSVNPG 322

RESULT 14

AAU80285
 ID AAU80285 standard; protein; 323 AA.

AC AAU80285;
 DT 30-JUL-2002 (first entry)
 XX
 DE Human IgE C2-C3-C4 domains for mammalian expression.
 XX
 KW IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
 KW antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;
 KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
 KW heavy chain C domain.

OS Homo sapiens.
 OS Synthetic.

XX WO200220038-A2.

XX 14-MAR-2002.

XX 06-SEP-2001; 2001WO-DK000579.

XX 06-SEP-2000; 2000DK-0000136.
 XX 15-SEP-2000; 2000US-0232831P.

PA (PHAR-) PHARMEXA AS.

XX Klyser S, Von Hoegen P, Voldborg B, Gautam A;

XX WPI, 2002-383033/41.

XX N-PSDB; AEX51133.

PT Inducing immune response against autologous immunoglobulin E in an
 PT animal, by effecting simultaneous presentation of cytotoxic T lymphocyte
 PT epitope and/or B-cell epitope derived from the immunoglobulin.

PS Disclosure, Page 108-110; 151pp; English.

XX
 XX This invention relates to a novel method for inducing an immune response
 CC against autologous immunoglobulin E (IgE) in an animal. The method
 CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte
 CC (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell
 CC epitope (TH epitope) which is foreign to the animal, by antigen
 CC presenting cells (APCs) of the animal's immune system. The epitopes of
 CC the invention may be used as a vaccine against allergic diseases. The
 CC method of the invention is useful for inducing an immune response against
 CC autologous IgE in an animal, which is useful for downregulating
 CC autologous IgE in the animal. This method is useful in the prevention and
 CC treatment of allergic diseases such as anaphylaxis, allergic rhinitis,
 CC asthma and atopic dermatitis. The present sequence represents the human
 CC IgE heavy chain C2-C3-C4 domains optimised for expression in a mammalian
 CC system, this sequence was used to create the epitopes of the invention
 XX
 SQ Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;
 Best Local Similarity 62.4%; Pred. No. 4,3e-78;
 Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;

QY 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTWLVGQEAENLFYTRPRKRG 81
 DB 6 PPTVKLIQSSCDGGHFPPTIQLCLVSGYTPGTINITWLBQVMD--VDLSTASTQ 63
 QY 82 GQTFSLQSEVNTQCGMSSNTYTCVYKNGSIFEDSRKCADSNPRGVSAVLSRPPFD 141
 DB 64 GELASTQSELTLSQKHWLSDRTYTQVYQGHTEFDSYRKCADSNPRGVSAVLSRPPFD 123
 QY 142 LFIKSPITTCVLDVLAASKGTVNLTWGRASGKPVNHSRKEKORNGTLVTSILPVG 201
 DB 124 LFIKSPITTCVLDVLAASKGTVNLTWGRASGKPVNHSRKEKORNGTLVTSILPVG 183
 QY 202 RDMWIGETVQCRVTHPHLPALMRSTYKLPGRALAPVYMLPSPDETGT--TRTVGLI 259
 DB 184 RDMWIGETVQCRVTHPHLPALMRSTYKLPGRALAPVYMLPSPDETGT--TRTVGLI 242
 QY 260 RGFYSEISVQWLFNNEBDHTGHTTTRPOKHGDPSPFLYSRLVKSIMWKNLVTVC 319
 DB 243 QNFMEEDISVQWLNHEVQLPDARHSTTOPRKTKS--GFVFSRLVTRAEWQKDEFTIC 300
 QY 320 RVVHEALPGSRTLEKSLHYSAG 341
 DB 301 RAVHEAASPSQTVQRAVSVNPG 322

RESULT 15

AAU80284
 ID AAU80284 standard; protein; 323 AA.

AC AAU80284;
 DT 30-JUL-2002 (first entry)
 XX
 DE Human IgE heavy chain C2-C3-C4 domains.
 XX
 KW IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
 KW antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;
 KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
 KW heavy chain C domain.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 11:57:11 ; Search time 45 Seconds
(without alignments)
2397.938 Million cell updates/sec

Title: US-09-401-636-8

Perfect score: 1856
Sequence: 1 EPHHHHHHTSLPESGPEVTI.....HEALPGSRTLEKSLHYSAGN 342

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_proteint:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	482.5	26.0	337	6	Q95M34 equus caball
2	479.5	25.8	473	4	Q8TC63 O8TC63 mus musculu
3	470	25.3	614	11	Q7TWT6 Q7TWT6 mus musculu
4	469	25.3	613	11	Q8VCX7 Q8VCX7 mus musculu
5	465	25.1	375	4	Q86TT1 Q86TT1 mus musculu
6	465	25.1	588	4	Q8WUX4 Q8WUX4 mus musculu
7	465	25.1	597	4	Q8BUI0 Q8BUI0 mus musculu
8	465	25.1	597	4	Q8BUI0 Q8BUI0 mus musculu
9	465	25.1	597	4	Q8BUI0 Q8BUI0 mus musculu
10	465	25.1	613	4	Q8WUX4 Q8WUX4 mus musculu
11	465	25.1	613	4	Q8WUX4 Q8WUX4 mus musculu
12	465	25.1	614	4	Q8WUX4 Q8WUX4 mus musculu
13	465	25.1	618	4	Q8WUX4 Q8WUX4 mus musculu
14	455	24.5	469	4	Q8WUX4 Q8WUX4 mus musculu
15	455	24.5	470	4	Q8WUX4 Q8WUX4 mus musculu
16	450	24.2	482	4	Q7Z351 Q7Z351 mus musculu

17	446	24.0	521	4	Q8N4Y9 Q8N4Y9 mus musculu
18	444	23.9	509	4	Q8N4Y9 Q8N4Y9 mus musculu
19	441	23.8	554	4	Q8N4Y9 Q8N4Y9 mus musculu
20	440.5	23.7	437	11	Q9R1A4 Q9R1A4 mus musculu
21	440	23.7	463	11	Q9R1A4 Q9R1A4 mus musculu
22	440	23.7	469	11	Q9R1A4 Q9R1A4 mus musculu
23	421	22.7	473	11	Q9R1A4 Q9R1A4 mus musculu
24	402.5	21.7	679	4	Q8D8L4 Q8D8L4 mus musculu
25	399	21.5	468	11	Q9R1A4 Q9R1A4 mus musculu
26	399	21.5	473	11	Q9R1A4 Q9R1A4 mus musculu
27	398	21.4	470	11	Q7TWT6 Q7TWT6 mus musculu
28	395.5	21.3	473	11	Q9R1A4 Q9R1A4 mus musculu
29	395.5	21.3	474	11	Q9R1A4 Q9R1A4 mus musculu
30	371.5	20.0	492	4	Q7Z374 Q7Z374 mus musculu
31	370.5	20.0	478	4	Q7Z374 Q7Z374 mus musculu
32	369.5	19.9	416	4	Q8N4Y9 Q8N4Y9 mus musculu
33	360	19.4	493	4	Q8N4Y9 Q8N4Y9 mus musculu
34	359	19.3	384	4	Q8N4Y9 Q8N4Y9 mus musculu
35	358	19.3	494	4	Q8N4Y9 Q8N4Y9 mus musculu
36	358	19.3	496	4	Q8N4Y9 Q8N4Y9 mus musculu
37	358	19.3	497	4	Q8N4Y9 Q8N4Y9 mus musculu
38	355.5	19.2	499	4	Q8N4Y9 Q8N4Y9 mus musculu
39	355.5	19.2	499	4	Q8N4Y9 Q8N4Y9 mus musculu
40	351.5	18.9	496	4	Q8N4Y9 Q8N4Y9 mus musculu
41	348	18.8	426	11	Q8N4Y9 Q8N4Y9 mus musculu
42	346	18.6	500	4	Q8N4Y9 Q8N4Y9 mus musculu
43	345	18.6	486	11	Q9R1A4 Q9R1A4 mus musculu
44	345	18.6	487	11	Q9R1A4 Q9R1A4 mus musculu
45	338.5	18.2	479	11	Q9R1A4 Q9R1A4 mus musculu

ALIGNMENTS

RESULT 1

Q95M34 PRELIMINARY: PRT; 337 AA.

AC Q95M34: 01-DEC-2001 (TREMUREL. 19, Created)

DT 01-DEC-2001 (TREMUREL. 19, Last sequence update)

DT 01-OCT-2003 (TREMUREL. 25, Last annotation update)

DE Immunoglobulin gamma 1 heavy chain constant region (Fragment).

GN IGHG1.

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OX NCBI_Taxid=9796;

RN (1)

RP SEQUENCE FROM N.A.

RA Wagner B.

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

RN (2)

RP SEQUENCE FROM N.A.

RX MEDLINE=98383416; PubMed=9717671;

RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,

RA Leibold W., Radbruch A.

RT "Organization of the equine immunoglobulin heavy chain constant region

RT genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes."

RL Immunobiology 199;105-119(1998).

DR EMBL, AJ300675; CAC44624.1..

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG-cl.

DR InterPro; IPR003006; IG_MHC.

DR Pfam; PF00047; Ig_2.

DR SMART; SM00407; IGH1, 2.

DR PROSITE; PS00835; IG_LIKE; 3.

DR PROSITE; PS00290; IG_MHC; 2.

FT NON_TER

SO SEQUENCE

Query Match 26.0%; Score 482.5; DB 6; Length 337;

Best Local Similarity 32.8%; Pred. No. 3.9e-36;

Matches 113; Conservative 67; Mismatches 120; Indels 45; Gaps 12;

QY 23 PTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW----LYDQGEANLFPYTTBP 78
 DB 6 PVFALADGCGTTS--STVALGCLVSGYFPEPVKSVNNGSLTSG--VHTFSPVL-- 57
 QY 79 REGGQFSLQSEVNITQCGMSSNTYTCHVKANGSIFE-----DSRRKCADSN--P 127
 DB 58 -QSSGFYLSMVTVPASTM--TSEYICNVVHAASNFVDRIRIPRIPNHCXVDMKCP 115
 QY 128 R-----GVSAVSRSPSPD-LFIRKSPITTCVVDLAPSKGTVNLWMSRAGKPVNH 178
 DB 116 KCPABELLGGSPVLFPPNPKDTLMTITPEVTCVVVDVSGQNDPVKFMWMDGVEVRA 175
 QY 179 STRKEKORNGTLVTTSTLPVGTDMIGETVQCRTHPHLPRALMRSTTLPGKRLAPE 238
 DB 176 TTRPEBQNSYRVRVSVLRIQHOMLSGKEFKCVNNOALPPIERTITTKRSQEPQ 235
 QY 239 VYMLPPSPBETGTR--TTCILIRGYPSEISVQMLFNNEDHTGHTTTRPQKHGTDPS 297
 DB 236 VYVLAHPHDELKSKSVATCVKDYFPEINIMESNQCPELETKYSITQAOCD--SDGS 293
 QY 298 FFLYSRLVYKSIWEKGNLVTGRVVEALPGSRITLKSLSHYSAGN 342
 DB 294 VFLYSKLSVDRNRMOGITTTCGVNHEALHN-----HTTQKN 330

RESULT 2

Q8TC63 PRELIMINARY; PRT; 473 AA.
 ID Q8TC63
 AC Q8TC63
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Kidney;
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC025985; AAH25985.1;
 DR GO; GO:0005489; F-actin binding; IEA.
 DR GO; GO:0005489; F-actin transport; IEA.
 DR GO; GO:0006118; P-selectin transport; IEA.
 DR InterPro; IPR000923; BlueCu.1.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_4.
 DR SMART; SM00406; IGV.1.
 DR PROSITE; PS00196; COPPER BLUE; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 473 AA; 51986 MW; E29920B9BA36F5 CRC64;

Query Match 25.8%; Score 479.5; DB 4; Length 473;
 Best Local Similarity 34.9%; Pred. No. 12e-35;
 Matches 120; Conservative 62; Mismatches 129; Indels 33; Gaps 11;

QY 18 VTIIPPTVK---LFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW----LYDQGEANL 70
 DB 142 VAVSPASTKGPSPVFLAPCSRSTSTALGCLVADYFPEPVWMSNGALTSG--VHT 198
 QY 71 FYYTRPRKRGQTFSLQSEVNITQCGMSSNTYTCHVKANGSIFE-----BDSRRKCADSNP-- 127
 DB 199 FPAVL---QSSGLYLSMVTVPASTM--TSEYICNVVHAASNFVDRIRIPRIPNHCXVDMKCP 253
 QY 128 -----RGVSAVSRSPSPD-LFIRKSPITTCVVDLAPSKGTVNLWMSRAGKPVNH 178

DB 254 SCPAPBFLGSPVFLFPPKPKDTLMTISRPBVTGVVDVSGQNDPVKFMWMDGVEVRA 313
 QY 179 STRKEKORNGTLVTTSTLPVGTDMIGETVQCRTHPHLPRALMRSTTLPGKRLAPE 238
 DB 314 KTRPREQNSYRVRVSVLTVLHOMLSGKEFKCVNNOALPPIERTITTKRSQEPQ 373
 QY 239 VYMLPPSPBETGTR--TTCILIRGYPSEISVQMLFNNEDHTGHTTTRPQKHGTDPS 297
 DB 374 VYVLAHPHDELKSKSVATCVKDYFPEINIMESNQCPELETKYSITQAOCD--SDGS 429
 QY 298 FFLYSRLVYKSIWEKGNLVTGRVVEALPGSRITLKSLSHYSAGN 341
 DB 430 FFLYSRLVYKSIWEKGNLVTGRVVEALPGSRITLKSLSHYSAGN 472

RESULT 3

Q7TM6 PRELIMINARY; PRT; 614 AA.
 ID Q7TM6
 AC Q7TM6
 DT 01-OCT-2003 (TREMblrel. 25, Created)
 DT 01-OCT-2003 (TREMblrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6NCr; Tissue=Hematopoietic Stem Cell;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
 RA Klausner R.D.; Collins F.S.; Wagner L.; Shemen C.M.; Schuler G.D.;
 RA Altschul S.F.; Zeeberg B.; Buelow K.H.; Scheef C.F.; Bhat N.K.;
 RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
 RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
 RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
 RA Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carroll J.; Prange C.;
 RA Baha S.S.; Loggiano N.A.; Peters G.J.; Abramson R.D.; Mullaly S.J.;
 RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gnatatone P.H.;
 RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
 RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
 RA Fahy J.; Helton E.; Kettelman M.; Madan A.; Rodriguez S.; Sanchez A.;
 RA Whiting M.; Madan A.; Young A.C.; Ruben A.C.; Bouffard G.G.;
 RA Blakeley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
 RA Rodriguez A.C.; Gilmwood J.; Schmitz J.; Myers R.M.; Butterfield Y.S.;
 RA Krzywiński M.I.; Skalska U.; Smalins D.E.; Scherch A.; Schein J.E.;
 RA Jones S.J.; Matra M.A.;
 RA "generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6NCr; Tissue=Hematopoietic Stem Cell;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC053409; AAH53409.1;
 KW Hypothetical protein.
 SQ SEQUENCE 614 AA; 67746 MW; 839BAF3BD124F89 CRC64;

Query Match 25.3%; Score 470; DB 11; Length 614;
 Best Local Similarity 34.1%; Pred. No. 1.3e-33;
 Matches 112; Conservative 57; Mismatches 139; Indels 20; Gaps 9;

QY 23 PTVKLFHSSCDPR---GDHSTIQLCLVSGSPAKVHTWLVQGEANLFPYTT 75
 DB 250 PAVNVF---VPPRDSGSPAPRKSILICATNFTFKPIVSWLKGKLVSGFTTDPVTL 306
 QY 76 RPRREGQTFSLQSEVNITQCGMSSNTYTCHVKANGSIFE-----BDSRRKCADSNPRAVSL 134
 DB 307 ENGSTPQTYKYSTLTITSEIDMLNVTYTCVDRGLFLKLVNSTCAASSTDLTFT 366
 QY 135 SRPSPDLFIRKSPITTCVVDLAPSKGTVNLWMSRAGKPVNHSTRKEKORNGTLT 194

```

Db 367 IPPSFADITLSKSNLTCVSNLATYE-TLNISWASOGSEPLETKIKIMESHPIGTSPAK 425
Qy 195 STLPGTRWIGETTYQCRVTHPHLPRALMRSTTLPGK--RLAEVYMLPPSEETG-- 250
Db 426 GVAACVEDMNRKKEVCTVTHRDLPSPQKFKISK-PNEVHGHPPAVYLLPPAREQNLRL 484
Qy 251 TTRVTCLIRGFYPSISVQWLFNNBEDHTGHTTRPQKHGTDPSFELSRMLVNSKI 310
Db 485 EBAITVCLVKGFSPADISVQWLRQGLLPQEKYVTSAMPBEGAGGFTHSILTVBEE 544
Qy 311 WEKGNLVTCRVVHEALP--GSRTLEKS 335
Db 545 WNSGETYTCVSHALPHLVTERTVDKS 572

```

RESULT 4

```

ID Q8VCX7 PRELIMINARY; PRT, 613 AA.
AC Q8VCX7;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
GN IGH-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018315; AAH18315.1; -.
DR MGI; MGI:96448; Igh-6.
DR InterPro; IPR007110; Igh-like.
DR InterPro; IPR003006; IGH_MHC.
DR InterPro; IPR003596; Igh_v.
DR Pfam; PF00047; Igh_5.
DR SMART; SM00406; Igh_1.
DR PROSITE; PS50835; IGH_LIKE; 5.
DR PROSITE; PS00290; IGH_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384D4C22862 CRC64;

```

Query Match 25.3%; Score 469; DB 11; Length 613;
 Best Local Similarity 34.1%; Pred. No. 1.6e-34;
 Matches 112; Conservative 57; Mismatches 139; Indels 20; Gaps 9;

```

Qy 23 PTVKLFHSSCDPR---GDAHSTIOLCLVSGSPAKVHTVWLVVGOEAEMLF---PYTT 75
Db 249 PAVNVF---VPRDGFSGAPRKSKLICEATNFTPKPTIVSILKDGKLVESGFTTDPVTI 305
Qy 76 RKRREGGQTFSLQSEVNTTQGMSSNTYTCVKNGSIF-EDSRKCAADSNPRGSAVYL 134
Db 306 ENKSGTPQTYKVISLTLTSEIDMLNLYTCVDRHGLTFLKNVSSSTCAASPTDILFTT 365
Qy 135 SRPSFDLFIKSPFTTCLVVDLAPSKGVNLTWGRASGKPVNSTRKEEQNRGLTVT 194
Db 366 IPPSFADITLSKSNLTCVSNLATYE-TLNISWASOGSEPLETKIKIMESHPIGTSPAK 424
Qy 195 STLPGTRWIGETTYQCRVTHPHLPRALMRSTTLPGK--RLAEVYMLPPSEETG-- 250
Db 425 GVAACVEDMNRKKEVCTVTHRDLPSPQKFKISK-PNEVHGHPPAVYLLPPAREQNLRL 483
Qy 251 TTRVTCLIRGFYPSISVQWLFNNBEDHTGHTTRPQKHGTDPSFELSRMLVNSKI 310
Db 484 EBAITVCLVKGFSPADISVQWLRQGLLPQEKYVTSAMPBEGAGGFTHSILTVBEE 543
Qy 311 WEKGNLVTCRVVHEALP--GSRTLEKS 335
Db 544 WNSGETYTCVSHALPHLVTERTVDKS 571

```

RESULT 5

```

ID Q86TT1 PRELIMINARY; PRT, 375 AA.
AC Q86TT1;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Human full-length cDNA clone C30DD006YL02 of neuroblastoma of Homo
DE sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Neuroblastoma;
RA Genoscope; (JAN-2003) to the EMBL/GenBank/DBJ databases.
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Neuroblastoma;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RL "Full-length cDNA libraries and normalization."
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX161420; CAD61894.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR007110; Igh-like.
DR InterPro; IPR003597; IGH_MHC.
DR InterPro; IPR003006; IGH_MHC.
DR Pfam; PF00047; Igh_3.
DR SMART; SM00407; Igh1_3.
DR PROSITE; PS50835; IGH_LIKE; 3.
DR PROSITE; PS00290; IGH_MHC; 3.
KW Plasmid.
SQ SEQUENCE 375 AA; 41272 MW; 7ACD1AF439C5EFC CRC64;

```

Query Match 25.1%; Score 465; DB 4; Length 375;
 Best Local Similarity 31.1%; Pred. No. 1.9e-34;
 Matches 105; Conservative 66; Mismatches 141; Indels 26; Gaps 11;

```

Qy 17 PVTII---PVTVLFIHSSCDPR---GDAHSTIOLCLVSGSPAKVHTVWLVVGOEAEMLF 69
Db 24 PLVIVALEPRKVSF---VPRDGFSGAPRKSKLICEATNFTPKPTIVSILKDGKLVESGFTTDPVTI 305
Qy 70 LFPTT-----RKRREGGQTFSLQSEVNTTQGMSSNTYTCVKNGSIF-EDSRKCA 123
Db 80 --GVTTDQVQAEKXSGSPPTTKVSTLTIKESDMVLSQSWFTRVDRHGLTFOQNASCKG 137
Qy 124 DSNPRGSAVLSRPSFDLFIKSPFTTCLVVDLAPSKGVNLTWGRASGKPVNSTRKE 183
Db 138 PDDDTAIRPAIPSPASIFLTKSTKLCLVVDLT-TYVSIVISWRQGEAVKHTNIS 196
Qy 184 EKQRNGTLVTVSTLPGTDMWIGETTYQCRVTHPHLPRALMRSTTLPGKRL-APVYML 242
Db 197 ESHPNATFSVGRASCEBDWNSGERFTCTVHTDLPSELKQTSIRPKVALHRPQVYLL 256
Qy 243 PSPEETG--TTRVTCLIRGFYPSISVQWLFNNBEDHTGHTTRPQKHGTDPSFEL 300
Db 257 PPAREQNLRLAESATITCLVKGFSPADISVQWLRQGLLPQEKYVTSAMPBEGAGGFTHS 316
Qy 301 YSHMLVNSKIWEKGNLVTCRVVHEALP--GSRTLEKS 335
Db 317 HSILTVSEEMNTGETTYCVVHVALPHLVTERTVDKS 571

```

RESULT 6

```

ID Q8WUX4 PRELIMINARY; PRT, 588 AA.
AC Q8WUX4;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)

```



```

CY 70 LFPYTT-----RPREGGQTFSLQSEVNITQGMSSNTYTCYKNGSIF-EDSSRKCA 123
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 302 --GVTIDVQVAAEAKESGPTTYKVTSTLTIKESDMLSGSMFTCVDRHGLTFQGNASMCV 359
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CY 124 DSNPRGVSAVLSRPSPPDLPIKSPPTTCLVLDIAPSKGTVNLTWSPASGKPVNHSTRKE 183
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 360 PDQDTAIRVFAIPSPFASIFLTSTKTLCTVTDLT--TVDSVTLSWTRONGEAVKHTNIS 418
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CY 184 EKQNGTLLTVSTLPVGRDWEIBETQOCRTVTHPLPALMRSTTKLPGRKL-APRYVYL 242
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 419 ESHNNAITSAVGEASICEDDMNSGERTCTVTHDLSPLKQITSRKGVALLRPDYLL 478
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CY 243 PPSPEETG--TTRVTCLIRGFYSEISVQMLFNNEEDHTGHTTTRPOKHGTDSPFL 300
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 479 PPARQJNLRESAITITCLVTFSPADVFVQMMQGRGQPLSPKRYTSAFMPBPQAPGRYFA 538
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CY 301 YSRMLVNSKIMEKGNLVTCRVVHEALPG---SRTLEKS 335
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 539 HSLITVSEEMWTGETTYTCAVAHEALPVRVTERIVDVS 576
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

RESULT 9

Q96BB9 PRELIMINARY; PRT; 597 AA.

```

AC Q96BB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Strauberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC015760; AAH15760.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_5.
DR SMART; SMO00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KM Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8EBC263D9 CRC64;

```

Query Match 25.1%; Score 465; DB 4; Length 597;
 Best Local Similarity 31.1%; Pred. No. 3.5e-34;
 Matches 105; Conservative 66; Mismatches 141; Indels 26; Gaps 11;

```

CY 17 PVTIT---PPTVKLFHSSCDPR---GDAHTIQLCLVSGFSPAKVHTVLDVQGAEN 69
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 246 PLPIVIAELPPIKVSF---VPPRDGFPGNPRKS-KLIQATGFSRQIOVSWLREGKOVGS 301
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CY 70 LFPYTT-----RPREGGQTFSLQSEVNITQGMSSNTYTCYKNGSIF-EDSSRKCA 123
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 302 --GVTIDVQVAAEAKESGPTTYKVTSTLTIKESDMLSGSMFTCVDRHGLTFQGNASMCV 359
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CY 124 DSNPRGVSAVLSRPSPPDLPIKSPPTTCLVLDIAPSKGTVNLTWSPASGKPVNHSTRKE 183
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 360 PDQDTAIRVFAIPSPFASIFLTSTKTLCTVTDLT--TVDSVTLSWTRONGEAVKHTNIS 418
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CY 184 EKQNGTLLTVSTLPVGRDWEIBETQOCRTVTHPLPALMRSTTKLPGRKL-APRYVYL 242
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 419 ESHNNAITSAVGEASICEDDMNSGERTCTVTHDLSPLKQITSRKGVALLRPDYLL 478
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CY 243 PPSPEETG--TTRVTCLIRGFYSEISVQMLFNNEEDHTGHTTTRPOKHGTDSPFL 300
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 479 PPARQJNLRESAITITCLVTFSPADVFVQMMQGRGQPLSPKRYTSAFMPBPQAPGRYFA 538
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

```

CY 301 YSRMLVNSKIMEKGNLVTCRVVHEALPG---SRTLEKS 335
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 539 HSLITVSEEMWTGETTYTCAVAHEALPVRVTERIVDVS 576
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

RESULT 10

Q96EYO PRELIMINARY; PRT; 613 AA.

```

ID Q96EYO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Strauberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC011857; AAH11857.1; -.
DR PIR; S15590; S15590.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_5.
DR SMART; SMO00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KM Hypothetical protein.
SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

```

Query Match 25.1%; Score 465; DB 4; Length 613;
 Best Local Similarity 31.1%; Pred. No. 3.7e-34;
 Matches 105; Conservative 66; Mismatches 141; Indels 26; Gaps 11;

```

CY 17 PVTIT---PPTVKLFHSSCDPR---GDAHTIQLCLVSGFSPAKVHTVLDVQGAEN 69
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 241 PLPIVIAELPPIKVSF---VPPRDGFPGNPRKS-KLIQATGFSRQIOVSWLREGKOVGS 296
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CY 70 LFPYTT-----RPREGGQTFSLQSEVNITQGMSSNTYTCYKNGSIF-EDSSRKCA 123
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 297 --GVTIDVQVAAEAKESGPTTYKVTSTLTIKESDMLSGSMFTCVDRHGLTFQGNASMCV 354
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CY 124 DSNPRGVSAVLSRPSPPDLPIKSPPTTCLVLDIAPSKGTVNLTWSPASGKPVNHSTRKE 183
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 355 PDQDTAIRVFAIPSPFASIFLTSTKTLCTVTDLT--TVDSVTLSWTRONGEAVKHTNIS 413
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CY 184 EKQNGTLLTVSTLPVGRDWEIBETQOCRTVTHPLPALMRSTTKLPGRKL-APRYVYL 242
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 414 ESHNNAITSAVGEASICEDDMNSGERTCTVTHDLSPLKQITSRKGVALLRPDYLL 473
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CY 243 PPSPEETG--TTRVTCLIRGFYSEISVQMLFNNEEDHTGHTTTRPOKHGTDSPFL 300
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 474 PPARQJNLRESAITITCLVTFSPADVFVQMMQGRGQPLSPKRYTSAFMPBPQAPGRYFA 533
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
CY 301 YSRMLVNSKIMEKGNLVTCRVVHEALPG---SRTLEKS 335
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 534 HSLITVSEEMWTGETTYTCAVAHEALPVRVTERIVDVS 571
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

RESULT 11

Q8WUK1 PRELIMINARY; PRT; 613 AA.

```

AC Q8WUK1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=tonsil;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC020240; AAH20240.1; -
 DR PIR; P10120; P10120.
 DR PIR; S15590; S15590.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 25.1%; Score 465; DB 4; Length 613;
 Best Local Similarity 31.1%; Pred. No. 3.7e-34;
 Matches 105; Conservative 66; Mismatches 141; Indels 26; Gaps 11;

CY 17 PVTII---PPTVKLFHSSCDPR---GDHSTIQLCLVSGSPAKYHVMVLDGQAEEN 69
 DB 241 PLPIVIAELPKVSVF---VPRDGFPGNPKRS-KLICQATGFSRQIQVSWLREGKQVGS 296
 CY 70 LFPYTT---RPKREGGQTSLSQEVNITOGQWMSNTTYCHYKNGSIF-EDSSRKCA 123
 DB 297 --GVTTDQVQAEAKSSGPTTYKVTSTLIKESDMLSQSMFTCRVDHRLTFQQAASMCV 354
 CY 124 DSNPRGVAAYLSRSPFLFTRKSPITICLVVDLAPSKGTNLTWSASGKPVNHSRKE 183
 DB 355 PDQDTAIRVFALPPSFASIFLTCKTKLCVTDLT-TYDSTISMTQNGEAVKTHNIS 413
 CY 184 EKQNGTLLVSTLPVGRDWIEGTYOCRYTHPHLPALMRSTTKLPGRKL-APEVYML 242
 DB 414 ESHPRATFSAVGEASICEDDNGSERFTCTVTHDLPSPKQITISRKGVALLRPDYLL 473
 CY 243 PPSPEETG--TTRVTCTLRGYPSEISVQWLFNNEBDHTGHHTTRPQDHTDPSFEL 300
 DB 474 PPARQQLMRBSATITCLVTGFSFADVFVQWQOGPLSPKRYTSAAPMPQAPGRYFA 533
 CY 301 YSRMLVNSIWEKGNLVCRVVHEALPG--SRITLKS 335
 DB 534 HSILTVSEEMNTGETTYCVVAHEALPVRVTERIVDKS 571

RESULT 12

096GA6 PRELIMINARY; PRT; 614 AA.

ID 096GA6
 AC 096GA6; 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC009851; AAH09851.1; -
 DR PIR; S15590; S15590.
 DR GO; GO:0005623; C:intracellular; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; F:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000005; HTHA1AC.

DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00041; HTH_APAQ_FAMILY_1, 1.
 DR PROSITE; PS00835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 614 AA; 67921 MW; 55BF536E77AA9BBB CRC64;

Query Match 25.1%; Score 465; DB 4; Length 614;
 Best Local Similarity 31.1%; Pred. No. 3.7e-34;
 Matches 105; Conservative 66; Mismatches 141; Indels 26; Gaps 11;

CY 17 PVTII---PPTVKLFHSSCDPR---GDHSTIQLCLVSGSPAKYHVMVLDGQAEEN 69
 DB 242 PLPIVIAELPKVSVF---VPRDGFPGNPKRS-KLICQATGFSRQIQVSWLREGKQVGS 297
 CY 70 LFPYTT---RPKREGGQTSLSQEVNITOGQWMSNTTYCHYKNGSIF-EDSSRKCA 123
 DB 298 --GVTTDQVQAEAKSSGPTTYKVTSTLIKESDMLSQSMFTCRVDHRLTFQQAASMCV 355
 CY 124 DSNPRGVAAYLSRSPFLFTRKSPITICLVVDLAPSKGTNLTWSASGKPVNHSRKE 183
 DB 356 PDQDTAIRVFALPPSFASIFLTCKTKLCVTDLT-TYDSTISMTQNGEAVKTHNIS 414
 CY 184 EKQNGTLLVSTLPVGRDWIEGTYOCRYTHPHLPALMRSTTKLPGRKL-APEVYML 242
 DB 415 ESHPRATFSAVGEASICEDDNGSERFTCTVTHDLPSPKQITISRKGVALLRPDYLL 474
 CY 243 PPSPEETG--TTRVTCTLRGYPSEISVQWLFNNEBDHTGHHTTRPQDHTDPSFEL 300
 DB 475 PPARQQLMRBSATITCLVTGFSFADVFVQWQOGPLSPKRYTSAAPMPQAPGRYFA 534
 CY 301 YSRMLVNSIWEKGNLVCRVVHEALPG--SRITLKS 335
 DB 535 HSILTVSEEMNTGETTYCVVAHEALPVRVTERIVDKS 572

RESULT 13

096GA6 PRELIMINARY; PRT; 618 AA.

ID 096GA6
 AC 096GA6; 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC017356; AAH17356.1; -
 DR PIR; S15590; S15590.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 618 AA; 67758 MW; 96DBDAC7C696E0A6 CRC64;

Query Match 25.1%; Score 465; DB 4; Length 618;
 Best Local Similarity 31.1%; Pred. No. 3.7e-34;
 Matches 105; Conservative 66; Mismatches 141; Indels 26; Gaps 11;

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QY 17 PVTII---PPTVTLFHSQDPR---GDASHITDLCVSGSPAKVHTW---LVGGEAENL 69
DB 246 PVPYIAELPKVSVF---VPRDGFPGNPKRS-KLICQATGSPRQIVSVLSRGGKQVS 301
QY 70 LEPTT-----RPRKGGQTFSEJSEVNIITGQOMMSNTYTCVHKGNSIT-EDSSKCA 123
DB 302 -GVTIDOVQAEAKSGGFTTYKVTITLTKESDMLTOSMFCRDRHRLTPOQNASMVCV 359
QY 124 DSNPRGVSAYLSRPSFDFLIRKSPITICLVVDLAPSKGTNLTWSRSGKPVNSTRKE 183
DB 360 PPOGTAIVFALPSPFASIFLTKSKTLCVLTDL-TYDSVTISWTRNGEAVKTHNIS 418
QY 184 EKORNGTLVSTLVEVGRDMIEGTYQCQRYTHPLPALMRSTTKLPGRKL-APRYTML 242
DB 419 ESHFATPSAVGEASICEDDMNSGERFTCTVTHDLPSPKQITSRPKGVALHPPDYLL 478
QY 243 PPSPRETG--TTRVTYCLIRGFPYPSISVOMLFNNEEDHTGHHTTRPOKDHGTDPSPFL 300
DB 479 PPARQMLNRESATITCLVGTSPADVFVQMMQROQPSPEKYTTSAPMPERQAPGRYFA 538
QY 301 YSRMLVNTSIMEKGNLVTCRVVHEALPG--SRILEKS 335
DB 539 HSILTVSEEWNTGETYTCVVAHEALPVRVTERVTDKS 576

RESULT 14
ID Q727P5 PRELIMINARY; PRT; 469 AA.
AC Q727P5;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=1477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., Loquellano N.A., Peters G.J., Adamson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman V.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,
RA Krzywnicki M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1; -.
KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51395 MW; CQD5BRI2BAAR795C CRC64;

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QY 18 VTIIPPTV---LFHSCDPRGDASHITDLCVSGSPAKVHTW---LVGGEAENL 70
DB 135 VIVSSASTGPGSVFPLPSPSKSTSGGTALGCLVADYFEPPTVMSNALSNG---VHT 191
QY 71 FPYTPRPRKGGQTFSEJSEVNIITGQOMMSNTYTCVHKGNSIT-EDSSKCA 120
DB 192 FPAVL-----QSSGLYSLSVTVTPSSS-LGTQTYICNVHKSNTKVDKVPKSCDKTH 246
QY 121 KC-----ADSNPRGVSAYLSRPSFDFLIRKSPITICLVVDLAPSKGTNLTWSRSGK 175
DB 247 TCPPCAPPELLGPPSVFLFPKPKOTLMSKPEYTCVAVDVSHEDPEKFNWYDGVAV 306
QY 176 VNHSTRKEKORNGTLVSTLVEVGRDMIEGTYQCQRYTHPLPALMRSTTKLPGRKL 235
DB 307 HNAKTPREEQYNSTFRVAVSVLTALHQPWLNGEKYKCKVSNALAPAPIEKTSKAKGQR 366
QY 236 APBYTMLPSPDEE-TCTTIVTYCLIRGFPYPSISVOMLFNNEEDHTGHHTTRPOKDHGT 294
DB 367 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMWSNQGEN-NYKTTTPVLD--S 422
QY 295 DPSFPLYSRMLVNTSIMEKGNLVTCRVVHEALPGSRILEKSHYAG 341
DB 423 DGSFPLYSKLTVDKSRMQQGNVFSQSVYHEALHNYT-QKSLSLSPG 468

RESULT 15
ID Q725W1 PRELIMINARY; PRT; 470 AA.
AC Q725W1;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=1477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., Loquellano N.A., Peters G.J., Adamson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman V.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,
RA Krzywnicki M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053984; AAH53984.1; -.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51204 MW; 778CF345214831EA CRC64;

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Query Match 24.5%; Score 455; DB 4; Length 469;
 Best Local Similarity 33.4%; Pred. No. 2.1e-33;
 Matches 116; Conservative 63; Mismatches 132; Indels 36; Gaps 12;

Query Match 24.5%; Score 455; DB 4; Length 470;
 Best Local Similarity 33.4%; Pred. No. 2.1e-33;

Matches 116; Conservative 63; Mismatches 132; Indels 36; Gaps 12;

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0Y 18 VTIIPFVVK---LFHSSCDPRGDASHITDLCUGVSGFPAKHVWY-----LYDQGEAENL 70
Db 136 VYSSASTKPSFPLPASPSTSGGTALGCLVDYDPEFVYVMSNGALTSG--VHT 1922
0Y 71 FPYTRPKRREGGOTFSLQSEVNIITOGQWMSNTYTCVHKHNGSIFE-----DSR 120
Db 193 FPAVL-----OSSGGLYSISSVYVTPSSS-LGTQTVICNVNHRKPSNXYDKKVEPKSCOKTH 247
0Y 121 KC-----ADSNPRGVSATLSRSPFD-LFRKSPITTCVLVDLAPSKGVMLTWGRASGKP 175
Db 248 TCPCCAPBELLGGPSVWFLFPPKXDTLMSRFBYTCVVDVSHDDPEVKKNWLYDGEV 307
0Y 176 VMSHTRKEEYQNRNGILTIVTSTLPEYGRDNIIBEGTYQCRVTHDPLPALMSRITYLPGRKL 235
Db 308 HNAKTKRREQYNSYTRVAVSVLVLMQDMLNKEKCYKSVSKNAPLPIEKTISPAKQPR 367
0Y 236 APEVYMLPPEPEE-TGTRTRVTCLIRGFPSSEISQWLFNNEEDTHGHTTRPOKHGT 294
Db 368 EPQVYTLFPRDELTINQVSLTCLVAGYFPRDIANWMSNQPEH--NYKTTTPVLD--S 423
0Y 295 DPEFLYSRLNKSIXWEKGLVTCVYVHEALPGSRITLKSLSHSAG 341
Db 424 DGSFELYSKLTVDKSRQOGNVSFSCVMEALHNHYT-QKSLISUSPG 469

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Search completed: February 26, 2004, 12:00:53
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 11:43:41 ; Search time 18 seconds
(without alignments)
989.333 Million cell updates/sec

Title: US-09-401-636-8

Perfect score: 1856
Sequence: 1 EFHHHHHTLSPSSGPVTI.....HEALPGSRTEKSLHYSAGN 342

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	1038.5	56.0	428 1 EPC_HUMAN	P01854 homo sapien
2	787.5	41.4	429 1 EPC_RAT	P01855 rattus norv
3	751	40.5	421 1 EPC_MOUSE	P06336 mus musculu
4	497.5	26.8	479 1 MUCB_MOUSE	P04221 cryocolagus
5	495.5	26.7	458 1 MUC_RABIT	P03988 cryocolagus
6	485.5	26.2	326 1 GC2_HUMAN	P01855 homo sapien
7	483	26.0	454 1 MUC_MESAT	P06337 mesocricetu
8	476	25.6	327 1 GC4_HUMAN	P01861 homo sapien
9	475.5	25.6	454 1 MUC_HUMAN	P01871 homo sapien
10	469	25.3	455 1 MUC_MOUSE	P01872 mus musculu
11	469	25.3	476 1 MUCB_MOUSE	P01870 mus musculu
12	460	24.8	391 1 MUCB_HUMAN	P04220 homo sapien
13	454	24.5	330 1 GCL_HUMAN	P01857 homo sapien
14	450	24.2	457 1 MUC_MOUSE	P07056 buncus murti
15	444	23.9	450 1 MUC_CANFA	P01874 canis famili
16	443.5	23.9	322 1 GEA_RAT	P20760 rattus norv
17	437.5	23.6	323 1 GC_RABIT	P01870 cryocolagus
18	436.5	23.5	326 1 GCL_RAT	P20762 rattus norv
19	428	23.1	329 1 GCC_RAT	P20763 rattus norv
20	424.5	22.9	329 1 GC2_MOUSE	P01865 cavia porce
21	421	22.7	335 1 GCAB_MOUSE	P01864 mus musculu
22	415.5	22.4	324 1 GCL_MOUSE	P01866 mus musculu
23	415.5	22.4	393 1 GCL_MOUSE	P01866 mus musculu
24	401.5	21.6	290 1 GCB_HUMAN	P01860 homo sapien
25	399.5	21.5	336 1 GCB_MOUSE	P01866 mus musculu
26	399.5	21.5	405 1 GCB_MOUSE	P01866 mus musculu
27	397	21.4	329 1 GCB_MOUSE	P22436 mus musculu
28	395.5	21.3	330 1 GCA_MOUSE	P01863 mus musculu
29	395.5	21.3	339 1 GCAM_MOUSE	P01865 mus musculu
30	392	21.1	398 1 GCB_MOUSE	P20767 mus musculu
31	384	20.7	333 1 GCB_RAT	P20767 rattus norv
32	371.5	20.0	438 1 HVC2_HETFR	P23085 heterodontu
33	369.5	19.9	340 1 ALC2_HUMAN	P01877 homo sapien

34	358	19.3	353 1 ALC1_HUMAN	P01876 homo sapien
35	352.5	19.0	438 1 HVCS_HETFR	P23087 heterodontu
36	352.5	19.0	461 1 HVCS_HETFR	P23088 heterodontu
37	348	18.8	353 1 ALC1_GORGO	P20758 gorilla gor
38	346.5	18.7	370 1 HVCI_HETFR	P23084 heterodontu
39	343.5	18.5	393 1 HVCI_HETFR	P23086 heterodontu
40	341	18.4	446 1 MDC_CHICK	P01875 gallus gall
41	335.5	18.1	344 1 ALC_MOUSE	P01878 mus musculu
42	277	14.9	481 1 MUCB_MOUSE	P23735 ictalurus p
43	260	14.0	299 1 ALC_RABIT	P01879 cryocolagus
44	227.5	12.3	383 1 DTC_HUMAN	P01880 homo sapien
45	167.5	9.0	503 1 SHS1_HUMAN	P78324 h protein-t

ALIGNMENTS

RESULT 1	ID	EPIC_HUMAN	STANDARD	PRT	428 AA.
AC	P01854	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	15 epsilon chain C region.				
GN	IGH.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE=8336887; PubMed=6300763;				
RA	Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,				
RA	Kikuchi M., Sugino Y., Nishida Y., Honjo T.;				
RT	"Molecular cloning and nucleotide sequencing of human immunoglobulin				
RT	epsilon chain cDNA."				
RL	Nucleic Acids Res. 11:719-726(1983).				
RN	[2]				
RP	SEQUENCE FROM N.A., AND VARIANT LEU-359.				
RX	MEDLINE=83001945; PubMed=6288268;				
RA	Max E.E., Battey J., Ney R., Kirsch I.R., Leder P.;				
RT	"Duplication and deletion in the human immunoglobulin epsilon genes."				
RL	Cell 29:691-699(1982).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=84236029; PubMed=6234164;				
RA	Flanagan J.G., Rabbits T.H.;				
RT	"The sequence of a human immunoglobulin epsilon heavy chain constant				
RT	region gene, and evidence for three non-allelic genes."				
RL	EMBO J. 1:655-660(1982).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=84207910; PubMed=6327276;				
RA	Ueda S., Nakai S., Nishida Y., Hisajima H., Honjo T.;				
RT	"Long terminal repeat-like elements flank a human immunoglobulin				
RT	epsilon pseudogene that lacks introns."				
RL	EMBO J. 1:1539-1544(1982).				
RN	[5]				
RP	PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND).				
RA	Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;				
RL	(in) Bach M.K. (eds.);				
RT	Immediate hypersensitivity: modern concepts and developments, pp.1-36,				
RL	Marcel Dekker, New York (1978).				
RN	[6]				
RP	SEQUENCE OF 1-40: 68-114 AND 427-428 FROM N.A.				
RX	MEDLINE=83065234; PubMed=6815656;				
RA	Karten U.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.;				
RA	Bell L.O., Gould H.U.;				
RT	"Cloning and sequence determination of the gene for the human				
RT	immunoglobulin epsilon chain expressed in a myeloma cell line."				
RL	Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).				
RN	[7]				

RP 3D-STRUCTURE MODELING.
 RX MEDLINE=87089848; PubMed=3796618;
 RA Padian E.A., Davies D.R.;
 RT "A model of the Fc of immunoglobulin E";
 RL Mol. Immunol. 23:1063-1075(1986).
 CC -1- SIMILARITY: Contains 4 immunoglobulin-like domains.
 CC -----
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 CC -----
 DR EMBL; I00022; AAB59424.1; ALT_INIT.
 DR PIR; A22771; EMTU.
 DR PDB; 1IG8; 15-JUL-92.
 DR PDB; 1FP5; 30-JAN-02.
 DR PDB; 1G84; 16-MAY-01.
 DR PDB; 1OOV; 18-SEP-02.
 DR Genew; HGNC:5522; IGHE.
 DR MIM; 147180; -.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00407; IgC1; 4.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 3.
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW 3D-structure; Repeat.
 FT NON_TER 1 1
 FT DOMAIN 6 103
 FT 103
 FT DOMAIN 112 210
 FT 210
 FT DOMAIN 214 318
 FT 318
 FT DOMAIN 324 423
 FT 423
 FT DISULFID 15 14
 FT 14
 FT DISULFID 15 105
 FT 105
 FT DISULFID 29 85
 FT 85
 FT DISULFID 121 121
 FT 121
 FT DISULFID 135 193
 FT 193
 FT DISULFID 209 209
 FT 209
 FT DISULFID 239 239
 FT 239
 FT DISULFID 345 405
 FT 405
 FT CARBOHYD 49 21
 FT 21
 FT CARBOHYD 99 49
 FT 49
 FT CARBOHYD 99 99
 FT 99
 FT CARBOHYD 146 146
 FT 146
 FT CARBOHYD 252 252
 FT 252
 FT CARBOHYD 275 275
 FT 275
 FT CARBOHYD 359 359
 FT 359
 FT VARIANT
 FT STRAND 110 110
 FT 110
 FT STRAND 113 117
 FT 117
 FT HELIX 122 124
 FT 124
 FT TURN 125 125
 FT 125
 FT STRAND 130 141
 FT 141
 FT STRAND 146 150
 FT 150
 FT STRAND 155 155
 FT 155
 FT STRAND 159 161
 FT 161
 FT STRAND 165 166
 FT 166
 FT TURN 168 169
 FT 169
 FT STRAND 172 181
 FT 181
 FT HELIX 182 186
 FT 186
 FT TURN 187 188
 FT 188
 FT STRAND 192 196
 FT 196
 FT TURN 198 199
 FT 199
 FT TURN 201 202
 FT 202
 FT STRAND 205 207
 FT 207
 FT STRAND 218 222
 FT 222

FT TURN 226 229
 FT TURN 231 232
 FT STRAND 236 242
 FT STRAND 252 252
 FT STRAND 255 257
 FT TURN 258 259
 FT STRAND 260 260
 FT TURN 265 266
 FT STRAND 271 274
 FT TURN 275 276
 FT STRAND 277 285
 FT TURN 288 293
 FT HELIX 294 294
 FT TURN 297 302
 FT STRAND 304 305
 FT TURN 310 314
 FT STRAND 322 322
 FT STRAND 325 329
 FT STRAND 334 337
 FT HELIX 334 348
 FT STRAND 340 348
 FT STRAND 350 351
 FT STRAND 356 360
 FT TURN 366 369
 FT STRAND 374 374
 FT STRAND 377 378
 FT TURN 380 381
 FT STRAND 384 385
 FT STRAND 387 393
 FT STRAND 394 398
 FT HELIX 394 400
 FT TURN 399 400
 FT STRAND 404 408
 FT STRAND 418 421
 FT STRAND 421 421
 SQ SEQUENCE 428 AA; 47019 MW; 25C4CA072AA558A0 CRC64;

Query Match 56.0%; Score 1038.5; DB 1; Length 428;
 Best Local Similarity 62.4%; Pred. No. 1.8e-72;
 Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;

22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKYHVMVLVDQEAENLFPYTRPKREG 81
 111 PPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKYHVMVLVDQEAENLFPYTRPKREG 168
 82 GQTFSLQSEVNTTQGMSSNTTTCYKANGSIFEDSSKCKDSNPRGVSAIATSPSPD 141
 169 GELASTQSEILTSQKMLSDRTTYQVYQGTFFEDSTKCKDSNPRGVSAIATSPSPD 228
 142 LFTKSPFTTCLVVDLAPSKGTVNLWSPASGPNVHSTRKEKORNGTLVTSILPVGT 201
 229 LFTKSPFTTCLVVDLAPSKGTVNLWSPASGPNVHSTRKEKORNGTLVTSILPVGT 288
 202 RDMIBETTYQCRVTHPLPRALMRSTTKLPGKRLAPEVYMLPPSPBETGT--TRVYTCII 259
 289 RDMIBETTYQCRVTHPLPRALMRSTTKLPGKRLAPEVYAF--ATPEWPSRDKRLACII 347
 260 RGFYPSFISVQWLFNNEEDHTGHTTTRPOKHGTDPSFLYSRLVNVKSIMKGNLVYC 319
 348 QNFMPEDISVQWLNHNEVQLPDARHSTTPKRTKGS--GFVFSRLVTRAEKQDEFIC 405
 320 RVVHEALPGSRITLKSILHYSAG 341
 406 RAVHEAASPGQTVQRAVSVPNG 427

RESULT 2
 EPC_RAT
 ID EPC_RAT STANDARD, PRT, 429 AA.
 AC P01855;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig epsilon chain C region.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 [1]
 RP SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2).
 RC STRAIN=LOU/C/MSL;
 RX MEDLINE=83064537; PubMed=6292865;
 RA Hellman L., Petersen U., Engstroem A., Karlsson T., Bennich H.;
 RT "Structure and evolution of the heavy chain from rat immunoglobulin
 E.";
 RL Nucleic Acids Res. 10:6041-6049(1982).
 RN [2]
 RP SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).
 RX MEDLINE=83182019; PubMed=6820340;
 RA Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;
 RT "A cloned cDNA probe for rat immunoglobulin epsilon heavy chain:
 RT construction, identification, and DNA sequence.";
 RL DNA 1:335-343(1982).
 RN [3]
 RP SEQUENCE OF 205-306 FROM N.A.
 RX MEDLINE=82174576; PubMed=6803238;
 RA Hellman L., Petersen U., Bennich H.;
 RT "Characterization and molecular cloning of the mRNA for the heavy
 RT (epsilon) chain of rat immunoglobulin E.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).
 CC -1- SIMILARITY: Contains 4 immunoglobulin-like domains.
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 CC
 CC EMBL; J00744; AAA41379.1; ALT_INIT.
 DR PIR; A93442; EHRT.
 DR HSSP; P01854; 1IGB.
 DR InterPro; IPR007110; Ig_1like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig1.
 DR SMART; SM00407; Igct1.1.
 DR PROSITE; PSS0835; Ig_1like; 4.
 DR PROSITE; PS00290; Ig_MHC; 3.
 KW Immunoglobulin domain; Immunoglobulin C region; Repeat.
 FT NON TER 1 1
 FT DOMAIN 1 89 IG-LIKE 1.
 FT DOMAIN 103 201 IG-LIKE 2.
 FT DOMAIN 205 305 IG-LIKE 3.
 FT DOMAIN 314 414 IG-LIKE 4.
 FT CONFLICT 168 168 R -> N (IN REF. 2).
 FT CONFLICT 308 308 P -> L (IN REF. 2).
 SQ SEQUENCE 429 AA; 48671 MW; D2970B34EFBA72B0 CRC64;

Query Match 41.4%; Score 767.5; DB 1; Length 429;
 Best Local Similarity 45.8%; Pred. No. 1,1e-51;
 Matches 151; Conservative 54; Mismatches 114; Indels 11; Gaps 4;
 QY 17 PVTIIPFVYKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHATWLVDCQEAENLPPYTR 76
 DB 97 PNIIRKPTVDLHSSCDPVA-PHSTIQLYCFYGHQIDVSHMLMDRKI-----YETH 150
 QY 77 PK-----REGGQTFSLQSEVNITQCGWMSNTYTGAVKNGSTFEDSSKCKADSNPRGVA 132
 DB 151 AONVLIKKEGKGLASTYSRLNITQCGWMSSTFTCKVTSQGENYMAHTRCSDDEPRGVIT 210
 QY 133 YLSRSPFDLFRKSPFTICLVVDLAPSKGVNLTWMSRAGKPVNHSRKEKQONGTLT 192
 DB 211 YLIPSPDLVYENGPKLCTCLVDL-ESEENITVWVAZERKKSIGSAQBSTKHNAITS 269
 QY 193 VTSILPVGTRDWIESETQOCRTVHPHLPALMRSTTKLPGKRLADEVTMLPPSPETGTT 252
 DB 270 ITSILPVAKDWIEBEGVQCRVDHDPFKPIVRSITKAPGRKSAPEVVFLLPPEEEKDK 329

RESULT 3
 EPC_MOUSE STANDARD; PRT; 421 AA.
 ID EPC_MOUSE
 AC P06336; P01856;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-1999 (Rel. 38, Last annotation update)
 DE Ig epsilon chain C region.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RP [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84236092; PubMed=6329728;
 RA Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;
 RT "The nucleotide sequence of the mouse immunoglobulin epsilon gene:
 RT comparison with the human epsilon gene sequence.";
 RL EMOB J. 1:1117-1123(1982).
 RN [2]
 RP REVISIONS.
 RA Honjo T.;
 RL Submitted (APR-1986) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 34-421 FROM N.A.
 RX MEDLINE=83117774; PubMed=6818553;
 RA Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;
 RT "Cloning and nucleotide sequence of mouse immunoglobulin epsilon
 RT chain cDNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).
 CC
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 CC
 CC EMBL; X01857; CA425977.1; -
 DR EMBL; X01857; CA425978.1; -
 DR PIR; A02144; EHMS.
 DR PIR; A02145; EHMS.
 DR HSSP; P01854; 1IGB.
 DR InterPro; IPR007110; Ig_1like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig1.
 DR SMART; SM00407; Igct1.2.
 DR PROSITE; PSS0835; Ig_1like; 4.
 DR PROSITE; PS00290; Ig_MHC; 3.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT NON TER 1 1
 FT DOMAIN 1 90 CH1.
 FT DOMAIN 91 197 CH2.
 FT DOMAIN 198 304 CH3.
 FT DOMAIN 305 421 CH4.
 FT DISULFID 23 75 BY SIMILARITY.
 FT DISULFID 121 180 BY SIMILARITY.
 FT DISULFID 226 285 BY SIMILARITY.
 FT DISULFID 330 392 BY SIMILARITY.
 FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 415 415 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 421 AA; 47320 MW; 8F909E1F30A06847 CRC64;

Query Match Best Local Similarity 40.5%; Score 751; DB 1; Length 421;
 Matches 155; Conservative 53; Mismatches 130; Indels 8; Gaps 4;

QY 2 FHHHHHTLSLPS-----GPTTTPYKLFHSSGCDPRGASHSTIOLCLVSGSPAKV 56
 DB 73 FICHVTHPPSPFNRSRTILVRPVNITEPTLEHSSCDPNA-FHSTIQLCYCFYGHILNDV 131
 QY 57 HTVWIDGGEAENLFYTRPRKGGQTSLSQVNTTQGMSSNTYTCVKNHNGSIFE 116
 DB 132 SYSLMDREBITDTLAQVLKEE-GKLASTCKMLTTEQOMSSSTFTCKVTSQGVYL 190
 QY 117 DSRKCADSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVALTWRSAGRPV 176
 DB 191 ATRRCPDHEPRGVITLYLPSPDLQNGAPKRLCLVVDLSEK-NVNVWNGEKTSTV 249
 QY 177 NHRSTRKBEKORNGTLVTSTLPVGRDMEGETYQCRVTHPHLPALMRSTTKLPKRLA 236
 DB 250 SASQWYTKHNNATSTISILPVADWIEGYQCTVDHPFPKPVASIKTKTGQSA 309
 QY 237 PEVYMLPSPPEETGTTRVTCILRGFPSEISVQWLFNNEEDHGHHTTRPOKHGDP 296
 DB 310 PEVYVPPPEESEDKRTITCLIQNFPEDISVQWLGQCKLSNOSHSTTPDKNSGNO 369
 QY 297 SPFLYSRLVYKSIWEKGLVTCRVVHEALPDSRTLEKSLHYSAGN 342
 DB 370 GFIFSRLEVAKTLWQKQFTCOVTHALQKPRLEKTIKSTISLN 415

RESULT 4
 MUCM RABIT STANDARD; PRT; 479 AA.

AC P04221;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 19 mu chain C region membrane-bound form.
 OS Oryctolagus cuniculus (Rabbit)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 ON NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A. (A2 ALLOTYPED).
 RX MEDLINE=84088930; PubMed=6418803;
 RA Bernstein K.E., Alexander C.B., Reddy E.P., Mage R.G.;
 RT "Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain
 of VHA2 allotype: comparisons with Vha1 and membrane mu sequences";
 RL J. Immunol. 132:490-495 (1984).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Purring differentiation, B lymphocytes switch from
 CC expression of isoform Membrane-bound to isoform Secreted;
 CC Name=Membrane-bound;
 CC IsoId=P04221-1; Sequence=Displayed;
 CC Name=Secreted;
 CC IsoId=P03988-1; Sequence=External;
 CC -----
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CC EMBL: K01357; AAA31293.1; --
 DR PIR: A02165; MRRBM.
 DR HSSP: P01842; 7PAB.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_4.
 DR SMART: SM00407; IgC1; 2.
 DR PROSITE: PS50835; IG_LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; 3.
 KM Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KM Alternative splicing; Transmembrane.
 FT NON TER 1
 FT DOMAIN 1 106 CH1.
 FT DOMAIN 107 222 CH2.
 FT DOMAIN 223 327 CH3.
 FT DOMAIN 328 458 CH4.
 FT TRANSMEM 459 476 CH4.
 FT DISULFID 14 14 POTENTIAL. (WITH LIGHT CHAIN) (PROBABLE).
 FT DISULFID 28 90 INTERCHAIN. (WITH HEAVY CHAIN) (PROBABLE).
 FT DISULFID 137 200 BY SIMILARITY.
 FT DISULFID 219 219 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
 FT DISULFID 249 308 BY SIMILARITY.
 FT DISULFID 296 296 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
 FT DISULFID 356 418 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 479 AA; 52351 MW; 689C637A47BE19FC CRC64;

Query Match Best Local Similarity 26.8%; Score 497.5; DB 1; Length 479;
 Matches 117; Conservative 61; Mismatches 153; Indels 25; Gaps 10;

QY 5 HHHHTLSLPSGPN-PIIPYVLFHSSGDP-----GDASHITQLCLVSGSPAKVHT 59
 DB 94 HSNRNDRVSPFVDELFPNVSVF--IPRDSFGSGSTRKRLICQATGSPKQISVS 150
 QY 60 WLVGGEAEN--LFYTRPRKGGQTSLSQVNTTQGMSSNTYTCVKNHNGSIFE 116
 DB 151 WLDGQGVESGVLTKEVBAETKAGPATFSISMLTTSMDLSGLYTCRVDRHGIFPD 210
 QY 117 DS---SRKCADSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVALTWRSAG 173
 DB 211 KNVSMSESGSTTSPSPDQVPLAPSPADPFLSKARLICLVTDLT-TYGSINIWSASHNG 269
 QY 174 KPVNHRSTRKBEKORNGTLVTSTLPVGRDMEGETYQCRVTHPHLPALMRSTTKLPK 233
 DB 270 KALDTMNTTSHSPNATFSMGEASVCADWDSGEFTVTHADLPFLKTKTIS--SR 327
 QY 234 KLA---PEVYMLPSPPEE--TGTRVTCILRGFPSEISVQWLFNNEEDHGHHTTRP 288
 DB 328 EVAKHPPAYVVLPPARQLVLRASATVTCLVGFSADVQVQORGGQLSDKVTSTAP 387
 QY 289 QKHGTDPSFLYSRLVYKSIWEKGLVTCRVVHEALP-----GSRTLEKSLHYSAG 341
 DB 388 APPQAPGLYFTHSTILVTEEDMNSGETFTCVVGHGHALPHMTERIVDSTGEV 443
 RESULT 5
 MUCM RABIT STANDARD; PRT; 458 AA.
 AC P03988;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 23-OCT-1986 (Rel. 02, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 19 mu chain C region secreted form.
 OS Oryctolagus cuniculus (Rabbit)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RL Mcl. Immunol. 16:923-925(1979).
 RN [17]
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Part D.M.
 RL Submitted (MAR-1980) to the PIR data bank.
 RN [18]
 RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=95255298; PubMed=7731190;
 RA Steppani M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.,
 RT "Disulphide bridges of the heavy chain of human anti-flavin monoclonal
 immunoglobulin";
 RL Biochem. J. 121:217-225(1971).
 RN [19]
 RP Bur. J. Biochem. 228:886-893(1995).
 RN [19]
 RP DISULFIDE BONDS.
 RX MEDLINE=72035500; PubMed=4940472;
 RA Milstein C., Frangione B.,
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 RN [10]
 RP DISULFIDE BONDS.
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Milstein C., Pink J.R.L.,
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
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 DR EMBL; J00230; AAB59393.1; -
 DR PIR; A93906; G2HU.
 DR HSSP; P01857; 1PCL.
 DR Genew; HGNC:5526; IGHG2.
 DR MIM; 147110; -
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding; TAG.
 DR GO; GO:0006555; F:immune response; NAS.
 DR InterPro; IPR007110; Ig-1like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; IGH1; 2.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KM Immunoglobulin domain; Immunoglobulin C region.
 FT NON TER 1 1
 FT DOMAIN 1 98 CHI.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT DISULFID 156 156
 FT SITE 326 326
 FT MOD RSS 326 326
 FT VARIANT 60 60
 FT CONFLICT 109 109 C -> S (IN REF. 3).
 FT SEQUENCE 326 AA; 35884 MW; 8310876C6878C9C CRC64;
 Query Match 26.2%; Score 486.5; DB 1; Length 326;
 Best Local Similarity 36.2%; Pred. No. 2,8e-30;
 Matches 117; Conservative 57; Mismatches 120; Indels 29; Gaps 11;

QY 35 RGAHSTIOLCTVSGSPAKVHTW----LVNQGAEHLFPYTRPRKREGQTFSLQSE 90
 DB 16 RSTESHTALGCLVYKDFPEPVVSNMNSGALNSG---VHTFAVL-----QSSGLATSLSSV 68
 QY 91 VNTGQGMSSNNTTGVKHA---NSIFEDSSRKCADSNP-----RGVAYLSRPSPF 140
 DB 69 VTPSSNF-GRQYTCVNDKRPENTKYDKVERKCCVCEPCPAPVAPSVFLFPPKPK 127
 QY 141 D-LFIRKSPITTCIVLDVLAISKGTVALTWSRASGKPVNSTKREKQKRGITVVTSTPV 199
 DB 128 DTLWISSTPEVTCVVDVSHEDPEVQFNWYGVGVHNAKTKPREQFNSTFRVSVTLTV 187
 QY 200 GTRWIEGTYQCYVTHPHLPAALASTYKLPKRLAPVYVLPSPPEP-TGTTTATVCL 258
 DB 188 VQDMLNGKRYCKVSKGLPAPLEKTSIKQPREPVYTLPSREEMTKNOVSLTCL 247
 QY 259 IRGFYPSRISYQMLFNNEDHTGHTTTPPOKDHGTPSPFPLYSRLYKKSIMKGNLVT 318
 DB 248 VKGFYPSDIAVEMNSQNPEN--NYKTPPMD--SDGSFFLYSKLTVDSKRWQGANVFS 303
 QY 319 CRVYHVALPGSRITLKSIAHSAG 341
 DB 304 CSVNHSLAHNYT-QKSLSLSPG 325
 RESULT 7
 MUC_MESAU STANDARD; PRT; 454 AA.
 AC P06337;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig mu chain C region.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85297761; PubMed=2994005;
 RA McGilre K.L., Duncan W.R., Tucker P.W.;
 RT "Phylogenetic conservation of immunoglobulin heavy chains: direct
 comparison of hamster and mouse Cmu genes.";
 RL Nucleic Acids Res. 13:5611-5628(1985).
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X02804; CAA26574.1; -
 DR HSSP; P01854; IIGB.
 DR InterPro; IPR007110; Ig-1like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00407; IGH1; 2.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 3.
 KM Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT NON TER 1 1
 FT DOMAIN 1 105 CHI.
 FT DOMAIN 106 218 CH2.
 FT DOMAIN 219 324 CH3.
 FT DOMAIN 325 454 CH4.
 FT DISULFID 13 13 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
 FT DISULFID 27 88 BY SIMILARITY.
 FT DISULFID 135 198 BY SIMILARITY.
 FT DISULFID 215 215 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 1-434 FROM N.A.
 RX MEDLINE=9032450; PubMed=2115996;
 RA Friedlander R.M., Nussenzweig M.C., Leder P.;
 RT "Complete nucleotide sequence of the membrane form of the human IGM
 heavy chain.";
 RL Nucleic Acids Res. 18:4278-4278(1990).
 RN [2]
 RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN GAL).
 RX MEDLINE=5059123; PubMed=4803843;
 RA Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
 RT "The primary structure of a monoclonal IGM-immunoglobulin
 (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
 type), subgroup H III. Architecture of the complete IGM-molecule.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
 RN [3]
 RP REVISIONS (GAL).
 RX MEDLINE=8106716; PubMed=6777162;
 RA Milnesco E., Barnikol-Watanabe S., Barnikol H.U., Milnesco C.,
 RA Hilschmann N.;
 RT "The primary structure of the constant part of mu-chain-disease
 protein BOT.";
 RL Eur. J. Biochem. 111:275-286(1980).
 RN [4]
 RP SEQUENCE (WALDENSTROM'S OU), DISULFIDE BONDS, AND CARBOHYDRATES.
 RX MEDLINE=74005511; PubMed=4742735;
 RA Putnam F.W., Florent G., Paul C., Shinoda T., Shimizu A.;
 RT "Complete amino acid sequence of the mu heavy chain of a human IGM
 immunoglobulin.";
 RL Science 182:287-291(1973).
 RN [5]
 RP PARTIAL SEQUENCE FROM N.A.
 RX MEDLINE=82059479; PubMed=6795593;
 RA Rablites T.H., Forster A., Milstein C.P.;
 RT "Human immunoglobulin heavy chain genes: evolutionary comparisons of
 C mu, C delta and C gamma genes and associated switch sequences.";
 RL Nucleic Acids Res. 9:4509-4524(1981).
 RN [6]
 RP SEQUENCE OF 299-387 AND 438-454 FROM N.A.
 RX MEDLINE=81077306; PubMed=6777778;
 RA Dolby T.W., Devuono J., Croce C.M.;
 RT "Cloning and partial nucleotide sequence of human immunoglobulin mu
 chain cDNA from B cells and mouse-human hybridomas.";
 RL Proc. Natl. Acad. Sci. U.S.A. 77:6027-6031(1980).
 CC -1- MISCELLANEOUS: All 4 combinations of the S/G and V/G polymorphisms
 at positions 192 and 216 have been observed in human mu chains.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X17115; CAA34971.1; ALT_SEQ.
 DR EMBL; X57086; -; NOT_ANNOTATED_CDS.
 DR HSSP; P01857; 1FCL.
 DR Gene; HGNC:5541; IGHN.
 DR MIM; 147020.
 DR GlycositeDB; P01871; -.
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00407; IgC1; 3.
 DR PROSITE; PS00835; IG_LIKE; 4.

DR PROSITE; PS00290; IG_MHC; 3.
 KM Immunoglobulin domain, Immunoglobulin C region; Glycoprotein;
 RN Polymorphism.
 FT NON_TER 1 1
 FT DOMAIN 1 105 CH1.
 FT DOMAIN 106 218 CH2.
 FT DOMAIN 219 324 CH3.
 FT DOMAIN 325 454 CH4.
 FT DISULFID 14 14 INTERCHAIN (WITH LIGHT CHAIN).
 FT DISULFID 28 88 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 135 198 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 215 215 INTERCHAIN (WITH HEAVY CHAIN IN ANOTHER
 FT DISULFID 245 304 SUBUNIT).
 FT DISULFID 292 292 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 352 414 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 453 453 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .).
 FT VARIANT 192 192 S -> G.
 FT VARIANT 192 192 /FTID=VAR_000219.
 FT VARIANT 216 216 /FTID=VAR_003903.
 FT VARIANT 216 216 V -> G (in dbSNP:12365).
 FT VARIANT 216 216 /FTID=VAR_003904.
 SQ SEQUENCE 454 AA; 49556 MW; 21BC72EAD056922E CRC64;
 Query Match 25.6%; Score 475.5; DB 1; Length 454;
 Best local similarity 31.4%; Pred. No. 3e-29;
 Matches 106; Conservative 65; Mismatches 142; Indels 25; Gaps 10;
 QY 17 PVTIT---PPTVGLFHSSCDPR---GDASTITGLCVSGSPAKVHTWTVDCQAEAN 69
 DB 102 PLRVIALPDKVSVF---VPRDGFGRNRSKLIQCATGSPQIQVSWLRGKQVGS 158
 QY 70 LFPYTT-----RKRRGGQTFISQSEVNITQGMSSNNTYGVKNGNSIF-EDSSRCKA 123
 DB 159 --GVTTIDQVQAKKEGSPPTTKVTSITLIKEDMWSQSFTRGVHRLGTFQNMSSMVCV 216
 QY 124 DSNPRGVSAVLSRSPFDLPIKSPFTTGLVVDLAPSKCTVNLWTSRPSGKFNSTKRE 183
 DB 217 PDODTARVFAIPSPASIFLTKESTLCTLVLDLT-TYSPVITSWTRONGEAVKHTNIS 275
 QY 184 EKQNGNGLVTVSTLPVGTDMTIGERTYQGRVTHPHLPALMRSSTKLPKRL-APGVNVL 242
 DB 276 ESHPNATFSAVGASACEDDWSGERFTCTVHTHTLPSLKQITGRPKVALHRDVIIL 335
 QY 243 PPSPEETG--TTRVTCLIRGYPSEISVQVLFNNEEDHTGHTTTPQKHGTDPSFL 300
 DB 336 PPARQQLNRESATITCLTGFSPADVFOVMQRGQPLSPKRYTSAPWEPQADGRYFA 395
 QY 301 YSRMLVNSIWMKGNLVTCRVVHVALPG---SRITLKS 335
 DB 396 HSLITVSSSRMNTGETTYTCVVAHEALPNRYTERIVDKS 433
 RESULT 10
 MUC_MOUSE STANDARD; PRT; 455 AA.
 AC P01872;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 19 mu chain C region secreted form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81076590; PubMed=6255422;


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CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=During differentiation, B lymphocytes switch from
CC expression of isoform Membrane-bound to isoform Secreted;
CC Name=Membrane-bound;
CC IsoId=P01873-1; Sequence=Displayed;
CC Name=Secreted;
CC IsoId=P01872-1; Sequence=External;
CC -!- MISCELLANEOUS: The sequence of residues 1-409 is assumed to be
CC identical with the corresponding region of the secreted form.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; V00821; CA24202.1; -
DR PIR; A01873; MEMM.
DR HSSP; P01873; 1FC1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00407; IgC1; 2.
DR PROSITE; PS50835; Ig_LIKE; 4.
DR PROSITE; PS00290; Ig_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; glycoprotein;
KW Alternative splicing; Transmembrane.
FT NON TER 1 1
FT DOMAIN 1 105 CH1.
FT 106 217 CH2.
FT 218 324 CH3.
FT 325 436 CH4.
FT TRANSMEM 456 473 POTENTIAL.
FT DISULFID 14 14 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
FT DISULFID 18 89
FT DISULFID 136 199 BY SIMILARITY.
FT DISULFID 216 216 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 246 305 BY SIMILARITY.
FT DISULFID 253 293 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 353 415 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .).
FT CARBOHYD 243 243 N-LINKED (GLCNAC. . .).
FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 476 AA; 52656 MW; 8D476575A5204071 CRC64;

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Query Match 25.3%; Score 469; DB 1; Length 476;

Best Local Similarity 34.1%; Pred. No. 9, 9e-29;

Matches 112; Conservative 57; Mismatches 139; Indels 20; Gaps 9;

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QY 23 PTVKLFHSSCDPR---GDAHSTIOLCLVSGFSPAKVHVMVLVDGQEAENL---PVT 75
DB 112 PAVNWF---VPRDGGSPAPRKSKLICEAINFTKXPITVSWLKGKGVESGFTTDPYTI 168
QY 76 RPKREGQTFSLQSEVNIITQOGMSSNTYTCVKNKNSIF-EDSSRKCADSNPRGSAVL 134
DB 169 ENKSGPTQYKVIISTLTISEIDMLNLYTCVDRGLTFKLVNSTCAASPSTDLFT 228
QY 135 SPSPPDLFIKSPPTTCLVLDLAPSKGVNLTMSRASKPVNSTRKEEQKQNTLVY 194
DB 229 IPSPADFLPSKANTCLVSNLAYE-TLNTSMASQSEPLETIKIMESHNPSTFAK 287
QY 195 STLPGVTRDMIGETVQCRVTHPHLPALMRSTKLPGK-RLAEVYMLPPSPETG-- 250
DB 288 GVASVCEVEDMNRKEKVCVTRDLPSPOKFKISK-PNEVHGKPPAVYLLPPARQNLAR 346
QY 251 TTRTVTCLIRGFYPSISVQWLFNNEEDHTGHTTTRPOKHGTDPSFVLSKMLYKSI 310
DB 347 ESATVTVCLVKGSPADISVQWLOKQLLPQEKVTSAPMPPEGADGFYFTHSILTVTEE 406

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QY 311 WEKGNLVTCRVVHEALP---GSRITLEKS 335
DB 407 WNSGERTVCVGHENALPHVYTERIVDKS 434

```

RESULT 12

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ID MUCB HUMAN STANDARD; PRT; 391 AA.
AC P04220;
DT 20-MAR-1987 (Rel. 04, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Ig mu heavy chain disease protein (BOT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=64184186; PubMed=6425189;
RA Barnikol-Watanabe S., Mhaesco E., Mhaesco C., Barnikol H.U.,
RA Hilschmann N.;
RT "The primary structure of mu-chain-disease protein BOT. Peculiar
RT amino-acid sequence of the N-terminal 42 positions.";
RL Hoppe-Seyler's Z. Physiol. Chem. 365:105-118(1984).
CC -!- MISCELLANEOUS: This protein has no V region homology or CH1
CC region.
DR PIR; A01873; MHRDUT.
DR HSSP; P01873; 1FC1.
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; P:antigen binding; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00407; IgC1; 2.
DR PROSITE; PS50835; Ig_LIKE; 3.
DR PROSITE; PS00290; Ig_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region.
KW FRB-C-PART (NO V REGION HOMOLOG).
FT DOMAIN 1 42
FT 43 155 CH2.
FT 156 261 CH3.
FT DOMAIN 262 391 CH4.
SQ SEQUENCE 391 AA; 43057 MW; 9100843AFC021A CRC64;

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Query Match 24.8%; Score 460; DB 1; Length 391;

Best Local Similarity 31.1%; Pred. No. 3, 8e-28;

Matches 105; Conservative 64; Mismatches 145; Indels 24; Gaps 11;

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QY 15 SGVPTI-IPPTVYKLFHSSCDPR---GDAHSTIOLCLVSGFSPAKVHVMVLVDGQEAEN 69
DB 40 SGVIAELPPKVSF---VPRDGGFPGNPKRS-KLICQATGSPQIEVSWLREGKQVGS 95
QY 70 LFPYTT-----RPRKREGQTFSLQSEVNIITQOGMSSNTYTCVKNKNSIF-EDSSRKA 123
DB 96 -GVTVDEVAEKESGPTTVKVTSTLTIKESDWMQGSVFTCRVHRLGTLTFQGNSSWCG 153
QY 124 DSNPRGVSAYLSRPSFDFIIRKSPITTCVLDLAPSKGVNLTMSRASKPVNSTRKEEQKQNTLVY 183
DB 154 PDQDTAIRFAIPPSASIFLTKSTLTCLVLDL-ITYSVITISWTRQDGAVKHTNIS 212
QY 184 EKQKNGTLVYSTLPGVTRDMIGETVQCRVTHPHLPALMRSTKLPGK-RLAEVYMLPPSPETG-- 242
DB 213 ESHPNATFAVAGASICEDWDGSEKFTVHTDLPFLKQITIRPKGVALLRPDVAVL 272
QY 243 PPSPEETG--TTRTVTCLIRGFYPSISVQWLFNNEEDHTGHTTTRPOKHGTDPSFVLSKMLYKSI 300
DB 273 PPARQNLNRESATITCLVTFSPADVQWVGQRPPEKVTYSAPMPPEGADGRYVA 332
QY 301 YSRMLYKSIWEKGNLVTCRVVHEALP---SRITLEKS 335

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DB 333 HSILFTVSEEMNTGETYTCVAHEALPNKVERTYDKS 370

RESULT 13
 ID GCI_HUMAN STANDARD; PRT; 330 AA.
 AC P01857;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE IG gamma-1 chain C region.
 GN IGHG1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82274238; PubMed=6287432;
 RA Ellison J.W., Berson B.D., Hood L.E.;
 RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
 RL Nucleic Acids Res. 10:4071-4079 (1982).
 RN [2]
 RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
 RX MEDLINE=71064024; PubMed=5489771;
 RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
 RT Wexler M.U., Edelman G.M.;
 RL "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
 RN [3]
 RP SEQUENCE OF 136-329 (EU).
 RX MEDLINE=71064025; PubMed=5530842;
 RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
 RT Edelman G.M.;
 RL "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
 RN [4]
 RP BIOCHEMISTRY 9:3171-3181 (1970).
 RX MEDLINE=7070269; PubMed=826475;
 RA Fostling H., Hilschmann N.;
 RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nle). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604 (1976).
 RN [5]
 RP SEQUENCE (MYELOMA PROTEIN KOL) AND DISULFIDE BONDS.
 RX MEDLINE=83289131; PubMed=6884994;
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747 (1983).
 RN [6]
 RP DISULFIDE BONDS.
 RX MEDLINE=71064027; PubMed=4923144;
 RA Gall W.E., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";
 RL Biochemistry 9:3188-3196 (1970).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=7070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nle). I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540 (1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;

RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from *Staphylococcus aureus* at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370 (1981).
 CC -1- MISCELLANEOUS: Nle has the G1M(17) allotypic marker, 97-K, and the G1M(1) marker, 239-D and 241-L. KOL and EU sequences have the G1M(3) marker and the G1M (non-1) marker.
 CC -1- MISCELLANEOUS: Nle also differs in the amidation states of 35, 116, 198, 269 and 272.
 CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues 155, 166, 177, 195, 198, 269, and 272 and in the order of residues 268-272.
 CC -1- MISCELLANEOUS: KOL also differs in the amidation states of residues 198, 267 and 272.
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 CC -----
 DR EMBL, J00228; AAC82527.1; AUT_INIT.
 DR PIR, A93433; GHHD.
 DR PDB, 1FC1; 15-JUL-92.
 DR PDB, 1FC2; 15-JUL-92.
 DR PDB, 1A77; 12-NOV-97.
 DR PDB, 1D58; 09-FEB-00.
 DR PDB, 1D57; 09-FEB-00.
 DR PDB, 1D6V; 04-OCT-00.
 DR PDB, 1DN2; 17-MAY-00.
 DR PDB, 1E4K; 06-JUN-01.
 DR PDB, 1FCC; 20-JUL-95.
 DR PDB, 1H2H; 12-JUN-02.
 DR PDB, 1I7Z; 08-AUG-01.
 DR PDB, 1IT5; 16-MAY-01.
 DR PDB, 1ITX; 16-MAY-01.
 DR PDB, 1L6X; 10-APR-02.
 DR PDB, 2RCS; 12-NOV-97.
 DR Genew; HGNC:5525; IGHG1.
 DR MIM; 147100; -.
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding; Tas.
 DR GO; GO:0006855; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR Pfam; PF00047; Ig_3.
 DR SMART; SM00407; IgG1; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KM Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KM 3D-structure.
 FT PT NON TER 1 1
 FT PT DOMAIN 1 98
 FT PT DOMAIN 99 110
 FT PT DOMAIN 111 223
 FT PT DOMAIN 224 330
 FT PT DISULFID 227 83
 FT PT DISULFID 103 103
 FT PT DISULFID 109 109
 FT PT DISULFID 112 112
 FT PT DISULFID 144 204
 FT PT DISULFID 250 308
 FT PT CARBOHYD 180 180
 FT MOD RES 330 330
 FT VARIANT 97 97
 FT VARIANT 239 239
 FT VARIANT 241 241
 N-LINKED (GLCNAC. . .).
 K -> R (IN G1M(3) MARKER).
 D -> E (IN G1M(NON-1) MARKER).
 /FTID=VAR 003886.
 L -> M (IN G1M(NON-1) MARKER).

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FT STRAND 122 126 /FTid=VAR_003888.
FT HELIX 130 134
FT TURN 136 137
FT STRAND 141 147
FT STRAND 157 162
FT TURN 163 164
FT STRAND 165 166
FT TURN 168 171
FT STRAND 176 179
FT TURN 180 181
FT STRAND 182 190
FT HELIX 193 197
FT TURN 198 199
FT STRAND 202 207
FT TURN 210 210
FT STRAND 215 219
FT STRAND 227 227
FT STRAND 230 234
FT HELIX 238 242
FT STRAND 245 256
FT STRAND 260 265
FT STRAND 270 276
FT STRAND 280 281
FT TURN 283 284
FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 305 312
FT TURN 313 314
FT TURN 316 317
FT STRAND 320 325
SQ SEQUENCE 330 AA; 36106 MW; 3770EB106C2F833D CRC64;

Query Match
Best Local Similarity 24.5%; Score 454; DB 1; Length 330;
Matches 117; Conservative 57; Mismatches 130; Indels 36; Gaps 12;

22 PPTVYKLFHSSCDPRGHAHTIOLCLVSGSPAKHYWV---LYDGEAEMLFPYTRP 77
6 PSYFPLAPSSKSTSG--STAALGCLVQDYFPEPTVWMSGALTSG--VHTPEAVL-- 57
78 KREGGQTFSLQSEVNTTQGWMSNTYTCHVKNHSIFE-----DSRRC-----A 123
58 --QSSGLYSLSSVTVPSSS-LGTQTYICNVHKSNTKVKVPEKSCDKHTCCPCPA 114
124 DSNPREVSAVLSRPSFD-LFTRKSPPTTCLVVDLAPKGVNLTWSASGKPVNHSRTR 182
115 PELLGGPSVFLPPPKXDTLMSRTPEVTCVAVDVSHEDEPKVKNWYVDGVEVNAKTKP 174
183 EERKQNGTLVTSTLPGTRDNI EGETYQCRVTHPLPALMRSTTKLPGKRLAPEVYM 242
175 REQVNSTRVVSVLVTHQDWLNGEKYCKVSNALPAPLEKITSKAKGQPREPVYTL 234
243 PPSPEE-TGHTRTVTCCLIRGFYPSSEISVQWLFNNEEDHTGHTTRPKQKHGTPSEFLY 301
235 PPRDELTLKQVSLTCLVKGFTPSDLAVMNSNGPEN--NYKTTPEVLD--SDGSFELY 290
302 SRMLVNSIKWEKGNLVTQCRVHEALPGSRTEKSLHYSAG 341
291 SKLTVDKSRWQGNVPSCSVMHEALHNHT--OKSLSLSPG 329

```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Soricidae; Crocidurinae; Suncus.
OC NCBI_Taxid=9378;
(1)
SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=89232144; PubMed=2497033;
RA Ishiguro H., Ichihara Y., Nankawa T., Nagatsu T., Kurosawa Y.;
RT "Nucleotide sequence of Suncus murinus immunoglobulin mu gene and
RT comparison with mouse and human mu genes.";
RL FEBS Lett. 247:317-322(1989).
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CC -----
CC EMBL, X13920; CAA32113.1; ALT_INIT.
CC PIR, S03961; S03961.
CC HSP, P01842; 7EAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00407; IgC1; 3.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; glycoprotein.
FT DOMAIN 1 105 CH1.
FT DOMAIN 106 220 CH2.
FT DOMAIN 221 326 CH3.
FT DOMAIN 327 457 CH4.
FT DISULFID 13 13 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
FT DISULFID 27 89 BY SIMILARITY.
FT DISULFID 136 200 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 217 217 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 248 307 BY SIMILARITY.
FT DISULFID 295 295 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 355 417 BY SIMILARITY.
FT CARBOHYD 456 456 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 457 AA; 50074 MW; 56C8C086DA446289 CRC64;

Query Match
Best Local Similarity 24.2%; Score 450; DB 1; Length 457;
Matches 105; Conservative 67; Mismatches 142; Indels 22; Gaps 9;

21 IPTVYKLFHSSCDPRGHAHTIOLCLVSGSPAKHYWV---LYDGEAEMLFPYTRP 75
110 LPNVSIF--VPRNSPSGNHPTSQLQASGFSRTTWSLDRGEVQSGVSTVISA 166
76 --RPRKGGQTFSLQSEVNTTQGWMSNTYTCHVKNHSIFE--SSRCKADSNPRGV 130
167 VEAEPKSGSPTTFVAVSRLLTTEBMLSGREFCOALHKLFLQKVVSVQMDDTSTGI 226
131 SAYLSRPSFDLFRKSPPTTCLVVDLAPKGVNLTWSASGKPVNHSRREKQRNGT 190
227 SVFLPPTFANIFLTQSAQLTCLVGTG--TYDSLDTSMSKQNEALQTHVNISESPNST 285
191 LVTSTLPGTRDNI EGETYQCRVTHPLPALMRSTTKLPGKRLA--PEVYMLPPSEP 247
286 FTAKGASVSCREWESEKFTCTVQSHDLSPKQISLR--PRQVANDPPSVFVLPAPQ 343
248 E--TGTRTVTCCLIRGFYPSSEISVQWLFNNEEDHTGHTTRPKQKHGTPSEFLYSRML 305

```

Db 344 QLKRESASITCLVKDSFDPVFNQGHGGQVDPDKHVTYNSNTPPEQNGLYFVHSILT 403
 QY 306 VNKSIEWKGNLVTCRVVHEALPGSRITLKSILHSAG 341
 Db 404 VSEKDWSSGESFSFCVVGHEALPLSLT-EKAVDKTSG 438

RESULT 15

MUC_CANFA STANDARD; PRT; 450 AA.
 ID MUC_CANFA
 AC P01874;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG mu chain C region.
 OS Canis familiaris (dog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_Taxid=9615;
 RN [1]
 RP SEQUENCE OF 1-177 (MOO).
 RX MEDLINE=80077682; PubMed=117299;
 RA "McCumber L.J., Capra J.D.;
 RT "The complete amino-acid sequence of a canine mu chain.";
 RL Mol. Immunol. 16:565-570(1979).
 RN [2]
 RP SEQUENCE OF 178-450 (MOO).
 RX MEDLINE=78180587; PubMed=653360;
 RA Wasserman R.L., Capra J.D.;
 RT "Amino acid sequence of the Fc region of a canine immunoglobulin M:
 RT interpectes homology for the IgM class.";
 RL Science 200:1159-1161(1978).
 DR PIR; A93131; MHDG.
 DR HSSP; P01857; IFCL.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00407; IGC1; 2.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON TER
 SQ SEQUENCE 450 AA; 48895 MM; 9D460DA9D1012F5D CRC64;

Query Match 23.9%; Score 444; DB 1; Length 450;
 Best Local Similarity 32.3%; Pred. No. 7.6e-27;
 Matches 111; Conservative 60; Mismatches 143; Indels 30; Gaps 13;

QY 10 LSLPE--SGPVTIIPFTVKLFHSSCDPRGDAHSTIQCLVSGFSPAKVHTW-LVDGQE 66
 Db 106 LTLPEVSG--FIPPRDAFPG--BPRKS-----QLICQASGFSPPGV--WSLRDGKQ 151
 QY 67 AENLPPTYT-----RPRREGQTFSLQSEVNITQGMSSNTYTCVKNENGSTP-EDSGR 120
 Db 152 IES--GYLTWEVVAZAZSGPTTYKVTSMLTIQDAWLSQVFCXKHEHRLTFOONASS 209
 QY 121 KCADSNPRGVSAYLSRPSFPDLFIKSPITICLVVDLAPSGKVTNLWMSRASGKPVNHS 180
 Db 210 MCTSDQPGVIGISITFIIPSPFASIFNTKSAKLSCLVTDLA-TYDSYITSWIRENGALKTH 268
 QY 181 RKEEKQKNGTLVTSTLPVGRDWIEGRTYQCRVTHPLPALMRSTTKLPGRKL-APEV 239
 Db 269 NISSEHPGRTPSAMGEATVCEWEESGQPFCTVTHDLPVLRKQTSRPGVAVHWPVS 328
 QY 240 YMLPSPPEGTG--TTRVTYCLIRGFYSEISVQWLFINNEBDHTGHHTTRPQKHGTDPS 297
 Db 329 YVLPSPRQGLDRSATSCLVYSGSPDVFTVQWQKQPPPPDSYVTSAPMPEPQAPGL 388
 QY 298 FFLYSRLVNKSIEWKGNLVTCRVVHEALPGSRITLKSILHSAG 341
 Db 389 YFAHSILTVSEEWNAGETVTCVVAHSLP-NRYTFRSVDKSTG 431

Search completed: February 26, 2004, 11:59:20
 Job time : 19 secs

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OM protein - protein search, using sw model

Run on: February 26, 2004, 11:45:31 ; Search time 20 Seconds
(without alignment)
1644.875 Million cell updates/sec

Title: US-09-401-636-8
Perfect score: 1856
Sequence: 1 EFHHHHHTSLPESGPVTL.....HEALPGSRLEKSLHYSAGN 342

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1038.5	56.0	428	1 EHHU	Ig epsilon chain C
2	1024.5	55.2	426	2 I36948	Ig epsilon chain C
3	767.5	41.4	429	1 EHTT	Ig epsilon chain C
4	751	40.5	388	1 EHTS	Ig epsilon chain C
5	682	36.7	548	2 S38864	Ig epsilon chain C
6	673	36.3	423	1 EHTS	Ig epsilon chain C
7	580.5	31.3	572	2 B46529	Ig epsilon chain C
8	535.5	28.9	504	2 S00390	Ig epsilon chain C
9	497.5	26.8	479	1 MHRBM	Ig mu chain C regi
10	496	26.7	454	1 MHRB	Ig mu chain C regi
11	495.5	26.2	458	1 MHRB	Ig mu chain C regi
12	486.5	26.2	326	1 G2HU	Ig gamma-2 chain C
13	480.5	25.9	343	2 S25644	Ig gamma-2 chain C
14	476	25.6	327	1 G4HU	Ig gamma-4 chain C
15	475.5	25.6	627	2 S14683	Ig gamma-4 chain C
16	473.5	25.5	328	2 I47161	Ig gamma-3 chain C
17	472	25.4	433	2 S31436	Ig gamma-3 chain C
18	469	25.3	455	1 MHRM	Ig gamma-3 chain C
19	469	25.3	455	1 A24976	Ig mu chain C regi
20	469	25.3	476	1 MHRM	Ig mu chain C regi
21	468	25.2	328	2 I47160	Ig gamma-2 chain C
22	465	25.1	328	2 I47159	Ig gamma-2 chain C
23	465	25.1	453	2 S37768	Ig mu chain C regi
24	465	25.1	453	2 S15590	Ig heavy chain - h
25	463.5	25.0	328	2 I47158	Ig gamma-1 chain C
26	460	24.8	391	1 MHRUBT	Ig mu heavy chain
27	458.5	24.7	592	2 S25705	Ig gamma-1 chain C
28	454	24.5	330	1 GHHU	Ig gamma-1 chain C
29	453.5	24.4	452	1 MHRU	Ig mu chain C regi

30	453.5	24.4	473	1 MHRUM	Ig mu chain C regi
31	450	24.2	457	2 S03961	Ig mu chain C regi
32	447	24.1	277	2 I47162	Ig gamma-4 chain C
33	447	24.1	377	2 A60764	Ig gamma-3 chain C
34	447	24.1	377	2 A23511	Ig gamma-3 chain C
35	446.5	24.1	374	2 S69339	Ig heavy chain V r
36	444	23.9	450	1 MHDG	Ig mu chain C regi
37	443.5	23.9	322	2 PS0019	Ig gamma-2a chain
38	440	23.7	472	2 S11459	Ig gamma-1 chain -
39	437.5	23.6	323	1 GHRB	Ig gamma chain C r
40	437.5	23.6	444	2 PC4436	monoclonal antibody
41	436.5	23.5	326	2 PS0017	Ig gamma-1 chain C
42	429	23.1	470	2 S22080	Ig heavy chain pre
43	428	23.1	329	2 S00847	Ig gamma-2c chain
44	428	23.1	549	2 S04845	Ig heavy chain pre
45	424.5	22.9	329	1 G2GP	Ig gamma-2 chain C

ALIGNMENTS

RESULT 1
EHHU
Ig epsilon chain C region - human
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1981 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
C/Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; C46
R/Flanagan, J.G.; Rabbitts, T.H.
EMBO J. 1, 655-660, 1982
A/Title: The sequence of a human immunoglobulin epsilon heavy chain constant region gene
A/Reference number: A22771; MUID:84236029; PMID:6234164
A/Accession: A22771
A/Molecule type: DNA
A/Residues: 1-428 <FLA>
A/Cross-references: GB:I00022; GB:J00227; GB:V00555; NID:g185035
R/Ueda, S.; Nakai, S.; Nishida, Y.; Hiseajima, H.; Honjo, T.
EMBO J. 1, 1539-1544, 1982
A/Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudog
A/Reference number: A23195; MUID:84207910; PMID:6327276
A/Accession: A23195
A/Molecule type: DNA
A/Residues: 2-428 <UED>
A/Cross-references: GB:J00222; NID:g184755
R/Zhang, K.; Saxon, A.; Max, E.E.
J. Exp. Med. 176, 233-243, 1992
A/Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing
A/Reference number: PH1214; MUID:92308839; PMID:1613458
A/Accession: PH1214
A/Molecule type: DNA
A/Residues: 320-428 <ZHA>
A/Cross-references: EMBL:X63693; GB:S38668; NID:g32987
R/Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Saesada, R.; Igarashi, K.; Kikuchi, M.; Sugi
Nucleic Acids Res. 11, 719-726, 1983
A/Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon cha
A/Reference number: A93491; MUID:83168897; PMID:6300763
A/Accession: A93491
A/Molecule type: mRNA
A/Residues: 1-428 <SEN>
A/Cross-references: GB:I00022; GB:J00227; GB:V00555; NID:g185035
R/Max, E.E.; Battey, J.; Ney, R.; Kirsch, I.R.; Leder, P.
Cell 29, 691-699, 1982
A/Title: Duplication and deletion in the human immunoglobulin epsilon genes.
A/Reference number: A90824; MUID:83001945; PMID:6288268
A/Accession: A90824
A/Molecule type: DNA
A/Residues: 1-358, 'L', 360-428 <MAX>
A/Cross-references: GB:J00222; NID:g184755
R/Bennet, H.H.; Johansson, S.G.O.; Von Bahr-Ulindstrom, H.
in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3
A/Reference number: A94418
A/Accession: A94418
A/Molecule type: protein

A:Residues: 'GAMTL',6,'X',8-16,'B',18-43,'B',45-52,55-92,95-97,'B',99-121,'B',123,'L',124
 A:Experimental source: myeloma protein Nd
 R:Kanten, J.H.; Mølgård, H.V.; Houghon, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G
 Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
 A:Title: Cloning and sequence determination of the gene for the human immunoglobulin epsilon
 A:Reference number: A53933; MUID:83065234; PMID:16815656
 A:Accession: B53933
 A:Molecule type: mRNA
 A:Residues: 1-40;68-114;427-428 <KEN>
 A:Cross-references: GB:100022; NID:G185035
 R:Ikeyama, S.
 FEBS Lett. 224, 306-310, 1987
 A:Title: Purification and characterization of a recombinant human IgE Fc-epsilon fragment
 A:Reference number: S02438; MUID:88083554; PMID:3121387
 A:Accession: S02438
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 98-352 <IKE>
 R:Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
 J. Biol. Chem. 269, 456-462, 1994
 A:Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces
 A:Reference number: A53116; MUID:94103254; PMID:8276835
 A:Accession: A53116
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 320-428 <ZH2>
 A:Experimental source: myeloma U266-derived cell line AF-10
 A:Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBI:141702)
 R:Hellman, L.
 Eur. J. Immunol. 23, 159-167, 1993
 A:Title: Characterization of four novel epsilon chain mRNA and a comparative analysis of
 A:Reference number: A46536; MUID:93122085; PMID:8419166
 A:Accession: C46536
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 382-426 <HEL>
 A:Cross-references: GB:S55273; NID:G263166; PIDN:AA24857.1; PID:G263167
 A:Experimental source: B cell myeloma U-266
 A:Note: sequence extracted from NCBI backbone (NCBIP:125297)
 A:Accession: D46536
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 382-391 <HE2>
 A:Cross-references: GB:S55276; NID:G263168; PIDN:AA24858.1; PID:G263169
 A:Experimental source: B cell myeloma U-266
 A:Note: sequence extracted from NCBI backbone (NCBIP:125299)
 A:Accession: A46536
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 401-428 <HE3>
 A:Cross-references: GB:S53497; NID:G263162; PIDN:AA24855.1; PID:G263163
 A:Experimental source: B cell myeloma U-266
 A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
 C:Genetics:
 A:Gene: GDB:IGHE
 A:Cross-references: GDB:119335; OMIM:147280
 A:Map position: 14q32.33-14q32.33
 A:Intron: 1/1; 104/1; 211/1; 319/1
 C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: alternative splicing; duplication; glycoprotein; heterotrimer; immunoglobulin F:128-195/Domain: immunoglobulin homology <IM1>
 F:128-195/Domain: immunoglobulin homology <IM2>
 F:1232-301/Domain: immunoglobulin homology <IM3>
 F:1338-401/Domain: immunoglobulin homology <IM4>
 F:14/Disulfide bonds: interchain (to light chain) #status predicted
 F:15-109,29-85,135-193,239-299,345-405/Disulfide bonds: #status predicted
 F:121,49,59,146,252,275/Binding site: carbohydrate (Asn) #status experimental
 F:121,209/Disulfide bonds: interchain (to heavy chain) #status predicted

Query Match 56.0%; Score 1038.5; DB 1; Length 428;
 Best Local Similarity 62.4%; Pred. No. 9.9e-71;

Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;
 QY 22 PPTVTKLFHSSCDPRGASHSTIOLCLVSGFSPAKVHTVLVDQEAENLFPYTRPREKRG 81
 DB 111 PPTVTKLFHSSCDPRGASHSTIOLCLVSGFSPAKVHTVLVDQEAENLFPYTRPREKRG 168
 QY 82 GQTFSLQSEVNTTQGMWMSNTYTCVKANGSIFEDSSKCKADSNRGVSAVLSRSPFD 141
 DB 169 GELASTQSELTLSQKMWLSDRITTCQVYQGHFEDSTKCKADSNRGVSAVLSRSPFD 228
 QY 142 LPIKSPITTCVVDLAPSGKTVNLTWASAGKPVNHSRKEKORNGTLVTSLPVGT 201
 DB 229 LPIKSPITTCVVDLAPSGKTVNLTWASAGKPVNHSRKEKORNGTLVTSLPVGT 288
 QY 202 RDMTGGTYQCRVTHPLPALMRSTTKLPGRKLAPVYMLPPSPETGT--TRVTCIL 259
 DB 289 RDMTGGTYQCRVTHPLPALMRSTTKLPGRKLAPVYMLPPSPETGT--TRVTCIL 347
 QY 260 RGFYPSISVQMLFNNEDHTGHTTRPOKHGTDPSFLYSRMVNSIWEKGNLYTC 319
 DB 348 QNFYPSISVQMLFNNEDHTGHTTRPOKHGTDPSFLYSRMVNSIWEKGNLYTC 405
 QY 320 RVVHEALPGSRTEKSLHYSAG 341
 DB 406 RVVHEALPGSRTEKSLHYSAG 427

RESULT 2

136948
 Ig epsilon-chain - chimpanzee (fragment)
 C:Species: Pan troglodytes (chimpanzee)
 C:Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
 C:Accession: 136948
 R:Sakoyama, Y.; Hong, K.
 Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
 A:Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orangute
 A:Reference number: 136948; MUID:8747136; PMID:3103123
 A:Accession: 136948
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-426 <RES>
 A:Cross-references: GB:M15398; NID:G176797; PIDN:AAA35416.1; PID:G176798
 C:Genetics:
 A:Introns: 103/1; 209/1; 317/1
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:1336-405/Domain: immunoglobulin homology <IM1>

Query Match 55.2%; Score 1024.5; DB 2; Length 426;
 Best Local Similarity 61.7%; Pred. No. 1.1e-69;
 Matches 198; Conservative 42; Mismatches 74; Indels 7; Gaps 4;
 QY 23 PTVTLFSSCDPRGASHSTIOLCLVSGFSPAKVHTVLVDQEAENLFPYTRPREKRG 82
 DB 110 PTVTLFSSCDPRGASHSTIOLCLVSGFSPAKVHTVLVDQEAENLFPYTRPREKRG 167
 QY 83 QTFSLQSEVNTTQGMWMSNTYTCVKANGSIFEDSSKCKADSNRGVSAVLSRSPFD 142
 DB 168 GELASTQSELTLSQKMWLSDRITTCQVYQGHFEDSTKCKADSNRGVSAVLSRSPFD 227
 QY 143 LPIKSPITTCVVDLAPSGKTVNLTWASAGKPVNHSRKEKORNGTLVTSLPVGT 202
 DB 228 LPIKSPITTCVVDLAPSGKTVNLTWASAGKPVNHSRKEKORNGTLVTSLPVGT 287
 QY 202 RDMTGGTYQCRVTHPLPALMRSTTKLPGRKLAPVYMLPPSPETGT--TRVTCIL 259
 DB 289 RDMTGGTYQCRVTHPLPALMRSTTKLPGRKLAPVYMLPPSPETGT--TRVTCIL 346
 QY 261 RGFYPSISVQMLFNNEDHTGHTTRPOKHGTDPSFLYSRMVNSIWEKGNLYTC 319
 DB 347 QNFYPSISVQMLFNNEDHTGHTTRPOKHGTDPSFLYSRMVNSIWEKGNLYTC 404
 QY 321 RVVHEALPGSRTEKSLHYSAG 341

Db 405 AVHBAASPQTVQRTVSVPNG 425

RESULT 3

EHRT

IG epsilon chain C region - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 17-Dec-1982 #sequence_revision 10-Dec-1982 #text_change 16-Jul-1999
 C/Accession: A93442; A90937; A02143
 R/Helms, L.; Petersen, U.; Engstrom, A.; Karlsson, T.; Bennich, H.
 Nucleic Acids Res. 10, 6041-6049, 1982
 A/Title: Structure and evolution of the heavy chain from rat immunoglobulin E.
 A/Reference number: A93442; MUID:83064537; PMID:6292865
 A/Accession: A93442
 A/Molecule type: mRNA
 A/Residues: 1-429 <HEL>
 A/Experimental source: Strain LOU/c/Mel, immunocytoma IR2
 R/Kindvogel, M.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.
 DNA 1, 335-343, 1982
 A/Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction,
 A/Reference number: A90937; MUID:83182019; PMID:6820340
 A/Accession: myeloma IR162
 A/Accession: A90937
 A/Molecule type: mRNA
 A/Residues: N, 169-307, L, 309-342 <KIN>
 C/Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 18 C/Superfamily: immunoglobulin C region; immunoglobulin homology
 C/Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin
 F/19-80/Domain: immunoglobulin homology <IM1>
 F/118-186/Domain: immunoglobulin homology <IM2>
 F/223-231/Domain: immunoglobulin homology <IM3>
 F/327-358/Domain: immunoglobulin homology <IM4>
 F/46,99,170,240,265,369,419/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 41.4%; Score 767.5; DB 1; Length 429;
 Best Local Similarity 45.8%; Pred. No. 2,66-50;
 Matches 151; Conservative 54; Mismatches 114; Indels 11; Gaps 4;

Db 17 PVTIIPPTVKLFHSCDPRGDAHSTIQLCLVSGSPAKYVTVLVGQAEMLFPYTR 76
 97 PVTITKPTVLDLHSSCPNA-FHSTIQLCFVYGHIONDSIHMLMDRKI-----YETH 150

Db 77 PK----REGQTFLOSQVNTTQGMSSNTYTCVKNHSIPESSKCADSNPQVSA 132
 151 AQNVLIKEEGKLAATSRKNTTQGMSSNTYTCVKNHSIPESSKCADSNPQVSA 210

Db 133 YLSRSPSPDLFIRKSPITTCVLDVLPASKGTVNLWTSRASKPVNSTRKEKQNGTLT 192
 211 YLIPSPDLVYENGPKLTCLVLDL-ESEENITVTVREKRSIGSASQSTGKHATTS 269

Db 193 VTSLPVTGTRMIGETTCQVTPHPLPALMRSTLPGKRLAPETVMLPSPBEETGT 252
 270 ITSLPVDKMWISGEQVDPHPKPVRTITAPGRSAPEVYVLPPEEEKDK 329

Db 253 RTVTCIRGFYPSISVQMLFNNEEDTGHHTTRPOKQDTPSEFYLRLVNSIWE 312
 330 RTVTCIRGFYPSISVQMLFNNEEDTGHHTTRPOKQDTPSEFYLRLVNSIWE 389

Db 313 KGNLVTCRVVHEALPGSRTELEKSLHYSAQN 342
 390 QTKQFTCRVTHLEALREPRKERTISKSLGN 419

RESULT 4
 EHMS
 IG epsilon chain C region (version 1) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 13-Jun-1993 #sequence_revision 13-Jun-1993 #text_change 16-Jul-1999
 C/Accession: A02144
 R/Li, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.
 Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982
 A/Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.

A/Reference number: A02144; MUID:83117774; PMID:6818553

A/Accession: A02144

A/Molecule type: mRNA

A/Residues: 1-388 <LID>

A/Cross-references: GB:J00476; NID:9194875; PIDN:AAA38085.1; PID:9387220

C/Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 18 C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin

F/1-44/Domain: immunoglobulin homology (fragment) <IM1>

F/81-149/Domain: immunoglobulin homology <IM2>

F/186-254/Domain: immunoglobulin homology <IM3>

F/290-361/Domain: immunoglobulin homology <IM4>

F/10,51,62,133,205,228,332,382/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 40.5%; Score 751; DB 1; Length 388;
 Best Local Similarity 44.8%; Pred. No. 4e-49;
 Matches 155; Conservative 53; Mismatches 130; Indels 8; Gaps 4;

Db 2 FHHHHHTLSLPEP-----GPVTIIPPTVKLFHSCDPRGDAHSTIQLCLVSGSPAKV 56
 40 FCHVTHPSPFESRTILVFPVNTIRPTELEHSSCPNA-FHSTIQLCFYGHINDV 98

Db 57 HTVAVDQGAENLFPYTRPRREGQTFPSIQSEVNTTQGMSSNTYTCVKNHSIFE 116
 99 SVSWMDREITDITLAQTVLKEE-GKLAATCSKLNTEQGMSSNTYTCVKNHSIFE 157

Db 117 DSSKCADSNPQVSAVYLSRSPDLFIRKSPITTCVLDVLPASKGTVNLWTSRASKPV 176
 158 AHTRCQPHRPGVITVILPSPDLVYNGAPKLTCLVLDLESEK-NVNVWNGEKTSV 216

Db 177 NHSTRKEKQNGTLVTVSTLPVGTROMISETTYQCRVTHPLPALMRSTTKLPQKLA 236
 217 SASQVTKHNNATTSITSLIPVAKMDIBYGVQCIYHDDPFPKPIRSTTKTPGQRSA 276

Db 237 PEVYMLPSPSEETGTRVTCIRGFYPSISVQMLFNNEEDTGHHTTRPOKQDTP 296
 277 PEVYMLPSPSEETGTRVTCIRGFYPSISVQMLFNNEEDTGHHTTRPOKQDTP 336

Db 297 SFYLSRMLVNSKIWEKGLVTCRVVHEALPGSRTELEKSLHYSAQN 342
 337 GFYLSRMLVNSKIWEKGLVTCRVVHEALPGSRTELEKSLHYSAQN 382

RESULT 5

IG epsilon chain C region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001

C/Accession: S38864

R/Kipp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library November 1993

A/Description: Combination of a defined specificity and desired isotype by cloning of ar

A/Reference number: S38864

A/Accession: S38864

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-548 <KIP>

A/Cross-references: EMBL:227397; NID:9416537; PIDN:CAA1768.1; PID:9340782

C/Superfamily: immunoglobulin C region; immunoglobulin homology

F/353-421/Domain: immunoglobulin homology <IM1>

Query Match 36.7%; Score 682; DB 2; Length 548;
 Best Local Similarity 43.0%; Pred. No. 9.6e-44;
 Matches 142; Conservative 52; Mismatches 122; Indels 14; Gaps 4;

Db 12 LPESGPVITIPPTVKLFHSCDPRGDAHSTIQLCLVSGSPAKYVTVLVGQAEML 69
 229 VPEVSVTFIPKPKP-----DVTIRSTIQLCFYGHINDVSVSWMDREITD 278

Db 70 LPPYTRPRRREGQTFPSIQSEVNTTQGMSSNTYTCVKNHSIFEPSKCADSNPQ 129
 279 TLAQTVLKEE-GKLAATCSKLNTEQGMSSNTYTCVKNHSIFEPSKCADSNPQ 337

Matches 118; Conservative 56; Mismatches 137; Indels 25; Gaps 10;

QY 17 PYTTPPTPKLPH-SSCDPRDASTIQLCLVSGSPAKVHTVLDGGAENLFPYTT 75
 Db 172 FVPVAPAPVQVLAHSSCP--SOSSEVLLCLVGFSPASAEVMDG--VGLVLAQ 227
 QY 76 RPKREGGQFSLQSEVNITQCGMMSNTYTCVHGH--NGSIFEDSRKCD--NPRG 129
 Db 228 SPARSGSTYLSLRVNVSGTDMREGKSYSCRVHPATNIVELHVGCCDGAQSCSP-- 285
 QY 130 VSAVLSRSPDPLTRKSPPTTCLVVDLAPSKGTVNLTWSPASGKPVNSTRKEKQNG 189
 Db 286 IQLVAIPSPGELIYISDAKRLCVLVMN--PSDSLSYTWTRKSGNLRPDMVLOEHFNG 344
 QY 190 TLVTSTLPVGTBMIEGETVQCRVTHGLPRALMRSTTKLPGKRLAPEVYMLPSPSEET 249
 Db 345 TYSASNAVPTQDMLSGERFCTVQHEELPLPSKSVYRNTGPTTLPPLPPAPHPPEL 404
 QY 250 GTTR-TVTCILRGFYPSEISVQMLFNNEDHTGHTTTPQKDH-----GTDPSFELY 301
 Db 405 SLSEVTLSCLVRGFRPRDIETIRMDRAVAPATEFTTAVLPEERTANGAGDGDTPFYV 464
 QY 302 SRMLVNSIWEKGNLVNCRVVAHP---GSRITLXK 334
 Db 465 SKMSVETAKMNGGVTFACMAVHEALPMRFSGRTLOK 500

RESULT 9

MBRM
 Ig mu chain C region, membrane-bound form - rabbit
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 04-Dec-1986 #sequence_revision 30-Jun-1991 #text_change 23-Aug-1997
 A/Accession: A02165; A02164
 R/Bernstein, K.E.; Alexander, C.B.; Reddy, E.P.; Magee, R.G.
 J. Immunol. 132, 490-495, 1984
 A/Title: Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain of V-Haz 8
 A/Reference number: A02164; MUID:8408930; PMID:6418803
 A/Contents: a2 allotype
 A/Accession: A02165
 A/Molecule type: mRNA
 A/Residues: 439-479 <BE2>
 A/Accession: A02164
 A/Molecule type: mRNA
 A/Residues: 1-438, 'GRPTLVNLSIMDSTASY' <BER>
 A/Note: the sequence of residues 1-438 was assumed to be identical with the corresponding C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16 C/Superfamily: immunoglobulin C region; immunoglobulin homology
 C/Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin
 F:21-92/Domain: immunoglobulin homology <IMM1>
 F:130-202/Domain: immunoglobulin homology <IMM2>
 F:242-310/Domain: immunoglobulin homology <IMM3>
 F:349-420/Domain: immunoglobulin homology <IMM4>
 F:439-479/Domain: carboxyl-terminal <CTS>
 F:14/Disulfide bonds: interchain (to light chain) #status predicted
 F:28-90, 137-200, 249-308, 356-418/Disulfide bonds: #status predicted
 F:46, 114, 261, 277, 284/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:219/Disulfide bonds: interchain (to heavy chain) #status predicted
 F:296/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted

Query Match 26.8%; Score 497.5; DB 1; Length 479;
 Best Local Similarity 32.9%; Pred. No. 6.4e-30;
 Matches 117; Conservative 61; Mismatches 153; Indels 25; Gaps 10;

QY 5 HHHTLSPESGPV-TIIPYTKLPHSSCDPR---GDAHSTIQLCLVSGSPAKVHT 59
 Db 94 HSNRDRLRVSPFVDSLPVSVF---IPRDSFGSGTKSKSLICQAGFSKQSVS 150
 QY 60 WLVNQGAEAN--LPIYTPRPGEGQTFSLQSEVNITQCGMMSNTYTCVHGH 116
 Db 151 WLRDQKVESGVLTIPVAEATKGAAPATFSSIMLTITSESDMLQSOJYTCVDRHGFFD 210
 QY 117 DS---SRKCADSNPRGSAVLSRSPDPLTRKSPPTTCLVVDLAPSKGTVNLTWSPASG 173

Db 211 KVVMSSECSSTPSPGICQVFIAPSPADTFISKARLCLVTDLT-TGSLNIMASANG 269
 QY 174 KPVNSTRKEKQNGRTLVSTLPEVGRDMLIEGTTCQRTVTHPLPALMRSTTKLPK 233
 Db 270 KALDTHMNTTESHNPATSNAMGEASVCAEDWESGQFTCTVHADLPPLKHTTSK--SR 327
 QY 234 RLA---PEVYMLPSPPEE--TGTRTVTCILRGFYPSEISVQMLFNNEDHTGHTTTP 288
 Db 328 EVAKIPPAVYVLPARQGLIRBSATVTCVKGSPADIVQMLQSGQPLSQKVTAP 387
 QY 289 QKHGTDSFPLYSKMLVNSIWEKGNLVNCRVVAHP---GSRITLXKSLHYSAG 341
 Db 388 APEQAPGLYFTHSTLVTVEEDNMGFTTCVVGHEALPMVTERTVKSGTEGVG 443

RESULT 10

MBRY
 Ig mu chain C region - golden hamster
 C/Species: Mesocricetus auratus (golden hamster)
 C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-1996
 A/Accession: A02168
 R/McGuire, K.L.; Duncan, W.R.; Tucker, P.W.
 Nucleic Acids Res. 13, 5611-5628, 1985
 A/Title: Phylogenetic conservation of immunoglobulin heavy chains: direct comparison of
 A/Reference number: A02168; MUID:85297761; PMID:2994005
 A/Accession: A02168
 A/Molecule type: DNA
 A/Residues: 1-454 <MCG>
 A/Note: the sequence was determined from the germline gene
 A/Note: the authors translated the codon GGT for residues 105 and 324 as Val and Glu re
 C/Genetics: 105/3; 218/3; 324/3
 C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16 C/Superfamily: immunoglobulin C region; immunoglobulin homology
 C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:20-90/Domain: immunoglobulin homology <IMM1>
 F:128-200/Domain: immunoglobulin homology <IMM2>
 F:238-306/Domain: immunoglobulin homology <IMM3>
 F:345-416/Domain: immunoglobulin homology <IMM4>
 F:445, 112, 139, 192, 210, 238, 257, 280, 326, 441/Binding site: carbohydrate (Asn) (covalent) #
 F:135-198, 245-304, 352-414/Disulfide bonds: #status predicted

Query Match 26.7%; Score 496; DB 1; Length 454;
 Best Local Similarity 34.5%; Pred. No. 7.8e-30;
 Matches 119; Conservative 60; Mismatches 150; Indels 16; Gaps 9;

QY 5 HHHT---LSLPSGPVTIIPYTKLPHSSCDP-RGDAHSTIQLCLVSGSPAKVHTV 60
 Db 91 HGNNTKDLRVADIPG-VTEMNPNVSVFVPSRDAFGAPRKSRLFCESANSFSPKQITVSW 149
 QY 61 LVNQGAEANL---PYTPRPGEGQTFSLQSEVNITQCGMMSNTYTCVHGHNSIF-E 116
 Db 150 LBDGKPVNSGFTPEVTPEDRSGRITKAVSTLITLTSDDLNSLVYICRDHRLGTLTK 209
 QY 117 DSSRKCADSNPRGSAVLSRSPDPLTRKSPPTTCLVVDLAPSKGTVNLTWSPASGKPV 176
 Db 210 NVSSITGAAPSRDIDAFPIPEPFVGIPLKSAITLCLVTNLA-TVDLTINISMSNGEPL 268
 QY 177 NSTRKEKQNGRTLVSTLPEVGRDMLIEGTTCQRTVTHPLPALMRSTTKLPK-KRL 235
 Db 269 ETKTKLTESHNPATSNAMGEASVCAEDWESGQFTCTVHADLPPLKHTTSKPGMKMT 328
 QY 236 APEVYMLPSPPEE--TGTRTVTCILRGFYPSEISVQMLFNNEDHTGHTTTPQKDH 293
 Db 329 PRAVYQQLPARQGLIRBSATVTCVKGSPADIVQMLQSGQPLSQKVTAPMRBPQ 388
 QY 294 TDSFPLYSKMLVNSIWEKGNLVNCRVVAHP---GSRITLXK 335
 Db 389 APHLVFTHSVLTVTVEEDNMGFTTCVVGHEALPMVTERTVKSGTEGVG 433

RESULT 11

MHRB

Ig mu chain C region, secreted form - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 23-Aug-1997

C/Accession: A02164

R/Accession: A02164

R/Reversion: K.E.; Alexander, C.B.; Reddy, E.P.; Mage, R.G.

J. Immunol. 132, 490-495, 1984

A/Title: Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain of V-Ha2 a

A/Reference number: A02164; PMID:8408930; PMID:6418803

A/Contents: a2 allotype

A/Accession: A02164

A/Molecule type: mRNA

A/Residues: 1-458 <ER>

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka)

hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1a

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob

F/130-202/Domain: immunoglobulin homology <IMM1>

F/242-310/Domain: immunoglobulin homology <IMM2>

F/349-420/Domain: immunoglobulin homology <IMM3>

F/14/Disulfide bonds: interchain (to light chain) #status predicted

F/28-90,137-200,249-308,356-418/Disulfide bonds: #status predicted

F/46,114,212,261,277,284,445/Binding site: carbohydrate (asn) (covalent) #status predict

F/219,457/Disulfide bonds: interchain (to heavy chain) #status predicted

F/296/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted

Query Match 26.7%; Score 495.5; DB 1; Length 458;

Best Local Similarity 33.1%; Pred. No. 8,6e-30;

Matches 116; Conservative 61; Mismatches 148; Indels 25; Gaps 10;

QY 5 HHHHTSLPESGQV--IIPIPTKLFHSSCDPR-----GDASHITOLCLVSGSPAKVYT 59

DB 94 HSNNDRLVSPFVDSLPNVSF--IPRDSGSGSTRKRIICQATGSPQJVS 150

QY 60 WLVDGQEAEN--LFPYTRPKREGQTFSLQSEVNTTGQWMSNTTYCHVKNISFE 116

DB 151 WLNDGQKVESGVLTKEVEAETKAGAPATFSSMLTTSSDWLSQSLVTCRDVHGIFPD 210

QY 117 DS---SRKCADSNPRVSAVLSRPPDLFIKSPITITLVYDLAPSKGTVNLTSRASC 173

DB 211 KVNMSSECSSTPSPQIQLPPLAPSPADTFYLSKARLILVLDL--TGSLSNTWSHNG 269

QY 174 KPVNSTRKREKORNTLTVTSTLPYGTDMWIEGTYQCRVTHPHLPALMSTKLPK 233

DB 270 KALDTMNTTSHPNATFSAWGASVCAEDWESGEFTCTVTHADLPPLKHTISK--SR 327

QY 234 RLA---PEVYMLPPSPFE--TGTRVYTCILRGTFYSLSVQWLNNEEDTHGHTTRP 288

DB 328 EVAKHPPAYVVLPAPEEQVLRASATVTLVKGFSADVFVWQORQGLSSDKYTSAP 387

QY 289 QXKHGDPSPFLYSRLVKNKSIWEKGNLTVCRVHAPL---GSRTLEKS 335

DB 388 APPQAPGLVTHSTILVTEBDNSETCTCVGHGHALPHMTERIVDS 437

RESULT 12

G2HU

Ig gamma-2 chain C region - human

C/Species: Homo sapiens (man)

C/Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000

C/Accession: A93906; A92809; A90752; A93132; A02168

R/Accession: A93906; A92809; A90752; A93132; A02168

R/Reversion: U. J. Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A/Title: linkage and sequence homology of two human immunoglobulin gamma heavy chain cor

A/Reference number: A93906; PMID:82197621; PMID:6804948

A/Accession: A93906

A/Molecule type: DNA

A/Residues: 1-326 <ELL>

A/Cross-references: GB:V00554; GB:J00230; NID:932759; PIDN:CA58438.1; PID:9606056

A/Note: Lys-326 is probably removed posttranslationally

R/Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A/Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and

A/Reference number: A92809; PMID:81007873; PMID:6774012

A/Contents: myeloma protein T11

A/Accession: A92809

A/Molecule type: protein

A/Residues: 1-119, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <MAN>

A/Note: TYP-156 is at or near the complement-binding site

R/Connell, G.E.; Parr, D.M.; Hofmann, T.

Can. J. Biochem. 57, 758-767, 1979

A/Title: The amino acid sequences of the three heavy chain constant region domains of a

A/Reference number: A90752; PMID:80001357; PMID:113060

A/Contents: myeloma protein Z1e

A/Accession: A90752

A/Molecule type: protein

A/Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198

A/Note: this sequence has since been revised

R/Hofmann, T.; Parr, D.M.

Mol. Immunol. 16, 923-925, 1979

A/Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin

A/Reference number: A93132; PMID:80114419; PMID:118920

A/Contents: Z1e

A/Accession: A93132

A/Molecule type: protein

A/Residues: 238-275 <HOP>

R/Hofmann, T.; Parr, D.M.

submitted to the Atlas March 1980

A/Reference number: A94591

A/Contents: annotation; Z1e, revisions to residues 25, 59, 60, and 264-268

A/Note: the revised sequence differs from that shown in having 60-Ala and in the amidat

ned

R/Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A/Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.

A/Reference number: A90253; PMID:72033500; PMID:440472

A/Contents: annotation; myeloma protein Sa, disulfide bonds

R/Frangione, B.; Milstein, C.; Pink, J.R.L.

Nature 221, 145-148, 1969

A/Title: Structural studies of immunoglobulin G.

A/Reference number: A93157; PMID:69064124; PMID:5782707

A/Contents: annotation; Sa, disulfide bonds

C/Genetics:

A/Gene: GDB:10H92

A/Cross-references: GDB:119338; OMIM:147110

A/Map position: 14q23.3-14q32.33

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka

hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F/20-85/Domain: immunoglobulin homology <IM1>

F/133-202/Domain: immunoglobulin homology <IM2>

F/233-306/Domain: immunoglobulin homology <IM3>

F/14/Disulfide bonds: interchain (to light chain) #status experimental

F/27-83,140-200,246-304/Disulfide bonds: #status experimental

F/107,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F/176/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 26.2%; Score 486.5; DB 1; Length 326;

Best Local Similarity 36.2%; Pred. No. 2.7e-29;

Matches 117; Conservative 57; Mismatches 120; Indels 29; Gaps 11;

QY 35 RGDASHITOLCLVSGSPAKVHTW---LVVQGAENLFPYTRPKREGQTFSLQSE 90

DB 16 RSTSESTALGLVQVFPFVTVSNKSLTIG---VHTFPAVL-----QSSGLVLSV 68

QY 91 VNITQGWMSNTTYCHVKH--NGSIFEDSKKCADSNP-----RGVSAYLSRPSPE 140

DB 69 VVVPSSNF--GTQVYTCVNDHKPSNTKVDKVERKCCVCEPCAPAPVAGSVLFPKPKR 127

QY 141 D-LFIRKSPITITGLVVDLAPSKGTVNLTWGRASGKPVNSTRKEKORNGTLVSTLPV 199

DB 128 DTLMISTRFEVYTCVVDVSHDEPVGPMVYDGVVHNAKTREREGFNSTFVSVLV 187

QY 200 GTRDWIEGETYQCRVTHPHLPALMRSTTKLPGKRLAPEVYMLPPSPPEE--TGTTRVTCTL 258
 DB 188 VHQMNLNKEKCKKCKVSNKGLPAPIEKTISKTKGQPREQVYTLTPSPSEMTKQVSLTCL 247
 QY 259 IRGYPSEISVQWLFNNEEDHTGHTTTPQKDHGTDPSPFLYSRMLVNSIWEKNLVLT 318
 DB 248 VKGFPSDIAVEMWESNGQPEN--NYKTPPMLD--SDGSFPLYSKLTVDKSRMOCQGVNFS 303
 QY 319 CRVYHEALPGSRITLTKSLHYSG 341
 DB 304 CSVMHEALHNYT--OKSLISLSPG 325

RESULT 13
 S25644
 Ig mu chain C region - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change 21-Jan-2000
 C:Accession: S25644
 R:Parkar, K.; Bugeon, L.; Soullieu, J.P.
 submitted to the EMBL Data Library, September 1992
 A:Reference number: S25644
 A:Accession: S25644
 A:Molecule type: mRNA
 A:Residues: 1-343 <PAR>
 A:Cross-references: EMBL:X68312; NID:G56461; PIDN:CAA6392.1; PID:9818025
 A:Experimental source: spleen
 C:Genetics:
 A:Map position: 6
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:234-305/Domain: immunoglobulin homology <IMM>

Query Match 25.9%; Score 480.5; DB 2; Length 343;
 Best Local Similarity 34.7%; Pred. No. 8e-29;
 Matches 108; Conservative 59; Mismatches 131; Indels 13; Gaps 7;

QY 36 GDAHSTIQLCLVGSFSPAKVHTVTLVGOEAENL---PYTPRKEGGQTFSLQSEVN 92
 DB 14 GPAPKSLICEATNFSKQITVSLQDQKFKGFTTEPYTVAKSRPQTVVISTLT 73
 QY 93 ITQGQWMSNTYTCVKNKNGSIF--EDSSRKCADSNPRGSAVLSRPSFPDLFIRKSPIT 151
 DB 74 ITESPMNLNVFTCVRDRLGFLFMKNVASTCAASPTDILAFPIPSPADIFLTKSAKLS 133
 QY 152 CLVVDLASKGTNVLTWRSASGKPVNSTRKEKQKQNGTLVTSTLTPGRDMTEGSTYQ 211
 DB 134 CLVTMLA-TYDTLNTSWSSKSGBLENTKIMESHNPSTFSAVGAASVCEDMDNRKEFV 192
 QY 212 CRVTHPHLPALMRSTTKLPGK--RLAPEVYMLPPSPPEE--TGTTRVTCTLIRGFYSEI 267
 DB 193 CLVTHRDLPSPQKRIK--PNEVAKHPAVYLLPAPRQQLIRSAVYTCCLVKFSPADL 251
 QY 268 SVQWLFNNEEDHTGHTTTPQKDHGTDPSPFLYSRMLVNSIWEKNLVTCRVYHEALP 327
 DB 252 FVQWLGQGPLSSDXYTSAPPEPGAGLYFTSHILTVTEEMNSEETVYCVVGHALP 311

QY 328 ---GSRITLTKS 335
 DB 312 HMYTERTVDKS 322

RESULT 14
 S14683
 Ig gamma-4 chain C region - human
 C:Species: Homo sapiens (man)
 C>Date: 02-Apr-1982 #sequence_revision 02-Apr-1992 #text_change 16-Jul-1999
 C:Accession: A90933; A90249; A02150
 R:Ellison, J.; Buxbaum, J.; Hood, L.
 DNA 1, 11-18, 1981
 A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
 A:Reference number: A90933; MUID:83157104; PMID:6299662
 A:Accession: A90933

A:Molecule type: DNA
 A:Residues: 1-327 <ELI>
 A>Note: the sequence was determined from the germline gene
 R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Melsestein, C.
 Biochem. J. 117, 33-47, 1970
 A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant
 A:Reference number: A90249; MUID:70207560; PMID:4192699
 A:Accession: A90249
 A:Molecule type: protein
 A:Residues: 1-30,81-326 <PIN>
 C:Genetics:
 A:Gene: GDB:IGHG4
 A:Cross-references: GDB:119340; OMIM:147130
 A:Map position: 14q32.33-14q32.33
 A:Introns: 99/1; 111/1; 221/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:20-85/Domain: immunoglobulin homology <IM2>
 F:134-203/Domain: hinge
 F:99-110/Domain: immunoglobulin homology <IM1>
 F:240-307/Domain: immunoglobulin homology <IM3>
 F:14/Disulfide bonds: interchain (to light chain) #status experimental
 F:27-83,141-201,247-305/Disulfide bonds: #status predicted
 F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
 F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.6%; Score 476; DB 1; Length 327;
 Best Local Similarity 35.8%; Pred. No. 1.7e-28;
 Matches 116; Conservative 57; Mismatches 121; Indels 30; Gaps 10;

QY 35 RGDASTIQLCLVGSFSPAKVHTV---LVGOEAENLFPYTPRKEGGQTFSLQSEVN 90
 DB 16 RSTSESTALGLVXDYEPPEPYTVWNSGALTSQ---VHTPAVL---QSSGLVLSLV 68
 QY 91 VNITQGWMSNTYTCVKNKNGSIFEDSSRKCADSNP-----RGVAVLSRSP 139
 DB 69 VIVPSS--LGTITTYCNVDHKSNTKVDKVESKTKGFPSCPAPEFLGSPVFLFPKP 127
 QY 140 PD-LPIRSPPTTCLVVDLAPSKGTNVLTWRSASGKPVNSTRKEKQKQNGTLVTSTLP 198
 DB 128 KDTLMSRTPPEVTCVVVVSQEDPEVQFVWYDVGEVNAATKPKPEEFGNSYRVAVSLT 187
 QY 199 VGRDWIEGETYQCRVTHPHLPALMRSTTKLPGKRLAPEVYMLPPSPPEE--TGTTRVTCT 257
 DB 188 VHQWNLNKEKCKKCKVSNKGLPSPSTIEKTSKAGQPREQVYTLTPSPSEMTKQVSLTCL 247
 QY 258 LIRGYPSEISVQWLFNNEEDHTGHTTTPQKDHGTDPSPFLYSRMLVNSIWEKNLV 317
 DB 248 LVKGFPSDIAVEMWESNGQPEN--NYKTPPMLD--SDGSFPLYSRLTVDKSRMOCQGVNFS 303
 QY 318 TCYVYHEALPGSRITLTKSLHYSG 341
 DB 304 CSVMHEALHNYT--OKSLISLSPG 326

RESULT 15
 S14683
 Ig mu chain precursor, membrane-bound (clone 201) - human
 C:Species: Homo sapiens (man)
 C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
 C:Accession: S14683; S08047
 R:Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
 Nucleic Acids Res. 18, 4278, 1990
 A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain
 A:Reference number: S14683; MUID:90332450; PMID:2115996
 A:Accession: S14683
 A:Molecule type: mRNA
 A:Residues: 1-627 <FRI>
 A:Cross-references: EMBL:X17115; NID:G33450; PIDN:CAA34971.1; PID:G33451
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin; membrane protein

